

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:18:56 ; Search time 50 Seconds  
(without alignments)  
950.583 Million cell updates/sec

Title: US-09-462-416A-7  
Perfect score: 2861  
Sequence: 1 MLVGCALLAALLAAPGAAL.....LILRSKFLOSSLRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pdp:\*  
2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pdp:\*  
3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pdp:\*  
4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pdp:\*  
5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCRUS COMB.pdp:\*  
6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pdp:\*  
7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1921	67.1	592	2	US-09-313-942-8
2	1921	67.1	592	2	US-10-282-162-8
3	1918	67.0	468	2	US-08-795-473B-5
4	1918	67.0	468	2	US-09-439-856-5
5	1918	67.0	468	2	US-09-949-016-5959
6	1918	67.0	468	7	5171840-2
7	1918	67.0	468	7	5480796-2
8	1910	66.8	360	2	US-09-313-942-15
9	1910	66.8	360	2	US-10-282-162-15
10	1852	64.7	344	7	5171840-7
11	1852	64.7	344	7	5480796-7
12	1788	62.5	1158	2	US-09-313-942-26
13	1788	62.5	1158	2	US-10-282-162-26
14	1783	62.3	1168	2	US-09-313-942-24
15	1783	62.3	1168	2	US-10-282-162-24
16	1741	60.9	323	7	5171840-6
17	1741	60.9	323	7	5480796-6
18	1683	58.8	315	2	US-09-313-942-16
19	1683	58.8	315	2	US-10-282-162-16
20	1481.5	51.8	388	2	US-09-949-016-9852
21	1389	48.5	386	7	5171840-5
22	1389	48.5	386	7	5480796-5
23	1153	40.3	210	2	US-09-043-785-1
24	950	33.2	201	7	5171840-11
25	939	32.8	185	1	US-08-716-317-7
26	938.5	32.8	212	1	US-08-792-019B-9

27	938.5	32.8	212	2	US-08-988-819-9	Sequence 9, Appli
28	938.5	32.8	212	2	US-09-016-534-9	Sequence 9, Appli
29	938.5	32.8	212	2	US-08-097-869-7	Sequence 7, Appli
30	938.5	32.8	212	2	US-08-795-473B-6	Sequence 6, Appli
31	938.5	32.8	212	2	US-09-230-637-45	Sequence 45, Appli
32	938.5	32.8	212	2	US-09-230-371A-27	Sequence 27, Appli
33	938.5	32.8	212	2	US-09-439-856-6	Sequence 6, Appli
34	938.5	32.8	212	2	US-09-462-941-13	Sequence 13, Appli
35	938.5	32.8	212	7	5510472-2	Patent No. 5510472
36	938.5	32.8	232	2	US-09-949-016-10315	Sequence 10315, A
37	935	32.7	317	2	US-08-469-318-145	Sequence 145, App
38	935	32.7	317	2	US-08-468-609A-145	Sequence 145, App
39	935	32.7	317	2	US-08-446-872A-145	Sequence 145, App
40	935	32.7	317	2	US-08-762-227A-145	Sequence 145, App
41	935	32.7	317	5	PCT-US95-01185-145	Sequence 145, App
42	934	32.6	184	1	US-08-567-047-2	Sequence 2, Appli
43	934	32.6	184	1	US-08-567-048-2	Sequence 2, Appli
44	934	32.6	184	7	5186931-1	Patent No. 5186931
45	934	32.6	185	1	US-07-632-070B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-313-942-8  
; Sequence 8, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-8

Query Match	67.1%	Score 1921;	DB 2;	Length 592;
Best Local Similarity	77.1%;	Pred. NO. 8.3e-151;		
Matches 377;	Conservative 22;	Mismatches 44;	Indels 46;	Gaps 5;
QY	1	MLVGCALLAALLAAPGAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60	
DB	1	MLVGCALLAALLAAPGAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60	
QY	61	VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEQLS	120	
DB	61	VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEQLS	120	
QY	121	CFKPSPLSNVVCWGPSTSLTTKAVLLVRKFKQNSPAEDFOEPCQYQSQKFSQCLAV	180	
DB	121	CFKPSPLSNVVCWGPSTSLTTKAVLLVRKFKQNSPAEDFOEPCQYQSQKFSQCLAV	180	
QY	181	PEGSSFFIVSMCVASSVGSFKSTQTFQGGILOPDPANITVTAVARNPRLSVTWOD	240	
DB	181	PEGSSFFIVSMCVASSVGSFKSTQTFQGGILOPDPANITVTAVARNPRLSVTWOD	240	
QY	241	PHSNSSFYRLRFEURYRAERSKTTTWMVKDQHQHCVIHDWAGSLRHVVQLRAQEEFQ	300	
DB	241	PHSNSSFYRLRFEURYRAERSKTTTWMVKDQHQHCVIHDWAGSLRHVVQLRAQEEFQ	300	
QY	301	GEWSWSPEAMGTPTWTESRPPAENEVSTPMQALTTNKDDONILFRDSANATSLPVEFMP	360	

Db 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 357  
Qy 361 VPPGSDSKDVAAPHROPLTSSRIDKQIRYILDGISALRKETCNKSNMCE--SSKEALAE 418  
Db 358 -----DAGEP-----KSCDKTHTCPPCPAPPELLGG 382  
Qy 419 NNLLPKMAEKDGCFCQGFNBETCLVKIIT---GLLEFEVYLEYQ---NRFESSEBOAR 472  
Db 383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 442  
Qy 473 AVQMSTKVL 481  
Db 443 STYRVSVL 451

RESULT 2  
US-10-282-162-8  
; Sequence 8, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-8

Query Match 67.1%; Score 1921; DB 2; Length 592;  
Best Local Similarity 77.1%; Pred. No. 8.3e-151;  
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MVAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTGHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTGHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCYSQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCYSQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITVAVARNRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITVAVARNRWLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEBFGQ 300  
Db 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEBFGQ 300  
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 357  
Db 361 VPPGSDSKDVAAPHROPLTSSRIDKQIRYILDGISALRKETCNKSNMCE--SSKEALAE 418  
Db 358 -----DAGEP-----KSCDKTHTCPPCPAPPELLGG 382  
Qy 419 NNLLPKMAEKDGCFCQGFNBETCLVKIIT---GLLEFEVYLEYQ---NRFESSEBOAR 472  
Db 383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 442

Qy 473 AVQMSTKVL 481  
Db 443 STYRVSVL 451

RESULT 3  
US-08-795-473B-5  
; Sequence 5, Application US/08795473B  
; Patent No. 6217858  
; GENERAL INFORMATION:  
; APPLICANT: Galun, Eithan  
; APPLICANT: Nahot, Orit  
; APPLICANT: Blum, Herbert E.  
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating  
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Davidson, Davidson and Kappel, LLC  
; STREET: 1140 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS-DOS EDITOR  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,473B  
; FILING DATE: 11-FEB-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Davidson, Clifford M.  
; REGISTRATION NUMBER: 32,728  
; REFERENCE/DOCKET NUMBER: 963.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)-997-1028  
; TELEFAX: (212)-997-1037  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
US-08-795-473B-5

Query Match 67.0%; Score 1918; DB 2; Length 468;  
Best Local Similarity 96.5%; Pred. No. 1e-150;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTGHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTGHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCYSQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCYSQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITVAVARNRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITVAVARNRWLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEBFGQ 300  
Db 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEBFGQ 300  
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 360

Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356

Qy 361 VPPGEDSKDVAAP 373  
Db 357 ----QDSSSVPLP 365

RESULT 4

US-09-439-856-5  
; Sequence 5, Application US/09439856  
; Patent No. 6410009  
; GENERAL INFORMATION:  
; APPLICANT: Galun, Eithan  
; APPLICANT: Nahot, Orit  
; APPLICANT: Blum, Herbert E.  
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating  
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Davidson, Davidson and Kappel, LLC  
; STREET: 1140 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS-DOS EDITOR  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/439,856  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/795,473  
; FILING DATE: 11-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Davidson, Clifford M.  
; REGISTRATION NUMBER: 32,728  
; REFERENCE/DOCKET NUMBER: 963.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)-997-1028  
; TELEFAX: (212)-997-1037  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
US-09-439-856-5

Query Match 67.0%; Score 1918; DB 2; Length 468;  
Best Local Similarity 96.5%; Pred. No. 1e-150;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;  
Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVRPEDNATVHW 60  
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVRPEDNATVHW 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVGSKFSKTQTQCGGILQDPDPANITVTAVARNPWLVSVTWOD 240  
Db 181 PEGDSSFYIVSMCVASSVGSKFSKTQTQCGGILQDPDPANITVTAVARNPWLVSVTWOD 240  
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTHWVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300  
Db 241 PHSWNSSFYRLRFELRYAERSKTFTHWVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Db 241 PHSWNSSFYRLRFELRYAERSKTFTHWVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300  
Qy 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVFEFMP 360  
Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356  
Qy 361 VPPGEDSKDVAAP 373  
Db 357 ----QDSSSVPLP 365

RESULT 5

US-09-949-016-5959  
; Sequence 5959, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5959  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5959

Query Match 67.0%; Score 1918; DB 2; Length 468;  
Best Local Similarity 96.5%; Pred. No. 1e-150;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;  
Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVRPEDNATVHW 60  
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVRPEDNATVHW 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVGSKFSKTQTQCGGILQDPDPANITVTAVARNPWLVSVTWOD 240  
Db 181 PEGDSSFYIVSMCVASSVGSKFSKTQTQCGGILQDPDPANITVTAVARNPWLVSVTWOD 240  
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTHWVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300  
Db 241 PHSWNSSFYRLRFELRYAERSKTFTHWVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300  
Qy 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVFEFMP 360  
Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356  
Qy 361 VPPGEDSKDVAAP 373  
Db 357 ----QDSSSVPLP 365

RESULT 6

5171840-2  
; Patent No. 5171840  
; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL  
; STIMULATORY FACTOR-2  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/298,694  
; FILING DATE: 19-JAN-1989  
; SEQ ID NO:2:  
; LENGTH: 468  
5171840-2

Query Match 67.0%; Score 1918; DB 7; Length 468;  
Best Local Similarity 96.5%; Pred. No. 1e-150;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300  
DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300

QY 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360  
DB 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

QY 361 VPPGEDSKOVAAP 373  
DB 357 ----QDSSSVPLP 365

RESULT 7  
5480796-2  
; Patent No. 5480796  
; APPLICANT: KISHIMOTO, TADAMITSU  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN  
; FOR HUMAN B CELL STIMULATORY FACTOR-2  
; NUMBER OF SEQUENCES: 8  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/907,650  
; FILING DATE: 02-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 298,694  
; FILING DATE: 19-JAN-1989  
; SEQ ID NO:2:  
; LENGTH: 468  
5480796-2

Query Match 67.0%; Score 1918; DB 7; Length 468;  
Best Local Similarity 96.5%; Pred. No. 1e-150;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300  
DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300

QY 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360  
DB 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

QY 361 VPPGEDSKOVAAP 373  
DB 357 ----QDSSSVPLP 365

RESULT 8  
US-09-313-942-15  
; Sequence 15, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 2; Length 360;  
Best Local Similarity 99.4%; Pred. No. 3.2e-150;  
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQDPPANNITVAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300  
DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFG 300

QY 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357  
DB 301 GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 9

US-10-282-162-15  
 ; Sequence 15, Application US/10282162  
 ; Patent No. 6927044  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203-B-US  
 ; CURRENT APPLICATION NUMBER: US/10/282,162  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 09/787,835  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045  
 ; PRIOR FILING DATE: 1999-09-22  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 15  
 ; LENGTH: 360  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-282-162-15

Query Match 66.8%; Score 1910; DB 2; Length 360;  
 Best Local Similarity 99.4%; Pred. No. 3.2e-150;  
 Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
 DB 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 DB 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 QY 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344  
 DB 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344

RESULT 10  
 5171840-7  
 ; Patent No. 5171840  
 ; APPLICANT: KISHIMOTO, TADAMITSU  
 ; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL  
 ; STIMULATORY FACTOR-2  
 ; NUMBER OF SEQUENCES: 11  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/298,694  
 ; FILING DATE: 19-JAN-1989  
 ; SEQ ID NO: 7;  
 ; LENGTH: 344  
 5171840-7

Query Match 64.7%; Score 1852; DB 7; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2e-145;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
 DB 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 DB 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 QY 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344  
 DB 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344

RESULT 11  
 5480796-7  
 ; Patent No. 5480796  
 ; APPLICANT: KISHIMOTO, TADAMITSU  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN  
 ; FOR HUMAN B CELL STIMULATORY FACTOR-2  
 ; NUMBER OF SEQUENCES: 8  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/907,650  
 ; FILING DATE: 02-JUL-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 298,694  
 ; FILING DATE: 19-JAN-1989  
 ; SEQ ID NO: 7;  
 ; LENGTH: 344  
 5480796-7

Query Match 64.7%; Score 1852; DB 7; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2e-145;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
 DB 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSOESOKFSCQLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTTFQGGCIGILQDPPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 DB 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
 QY 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344  
 DB 301 GEWSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLL 344

RESULT 12  
 US-09-313-942-26  
 ; Sequence 26, Application US/09313942  
 ; Patent No. 6472179  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.

```
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

Query Match      62.5%; Score 1788; DB 2; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.5e-139;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||

QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQAL 334
   :|||||
Db 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMELL 334
   :|||||

RESULT 13
US-10-282-162-26
; Sequence 26, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-26

Query Match      62.5%; Score 1788; DB 2; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.5e-139;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
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Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||

QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQAL 334
   :|||||
Db 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMELL 334
   :|||||

RESULT 14
US-09-313-942-24
; Sequence 24, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-24

Query Match      62.3%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 6.6e-139;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQSKFSCQLAV 180
   :|||||

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPPPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEBFGQ 300
   :|||||

QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPM 331
   :|||||
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301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPM 331

|||||  
Db 301 GEWSEWSPAMGTPWTEGRSPPAENEVSTPM 331  
  
RESULT 15  
US-10-282-162-24  
; Sequence 24, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 1168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-24  
  
Query Match 62.3%; Score 1783; DB 2; Length 1168;  
Best Local Similarity 99.7%; Pred. No. 6.6e-139;  
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLAVGCALLAALLAAPGALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60  
Db 1 MVAVGCALLAALLAAPGALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60  
  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPOL 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPOL 120  
  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQSQESQKFSQCLAV 180  
  
Qy 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGILOPDPANITVTAVARNPRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGILOPDPANITVTAVARNPRWLSVTWQD 240  
  
Qy 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGRLRHVVQLRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGRLRHVVQLRAQEEFGQ 300  
  
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Job time : 51 secs

11/11/11



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:30:56 ; Search time 181 Seconds  
(without alignments)  
1389.645 Million cell updates/sec

Title: US-09-462-416A-7  
Perfect score: 2861  
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSFKFLOSLRALRQM 543

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2772	96.9	569	5	US-10-485-545A-14
2	1921	67.1	592	3	US-09-313-942-8
3	1921	67.1	592	3	US-09-313-942-8
4	1921	67.1	592	4	US-10-287-035-8
5	1921	67.1	592	4	US-10-287-035-8
6	1921	67.1	592	6	US-11-134-114-8
7	1918	67.0	468	4	US-10-247-463-12
8	1918	67.0	468	5	US-10-756-149-5377
9	1918	67.0	468	3	US-09-313-942-15
10	1910	66.8	360	3	US-09-313-942-15
11	1910	66.8	360	3	US-09-935-868-15
12	1910	66.8	360	4	US-10-287-035-15
13	1910	66.8	360	4	US-10-282-162-15
14	1910	66.8	360	6	US-11-134-114-15
15	1902	66.5	468	5	US-10-485-545A-11
16	1897	66.3	357	5	US-10-485-545A-13
17	1891	66.1	364	5	US-10-485-545A-10
18	1891	66.1	365	5	US-10-485-545A-12
19	1823.5	63.7	453	4	US-10-322-696-144
20	1788	62.5	1158	3	US-09-313-942-26
21	1788	62.5	1158	3	US-09-935-868-26
22	1788	62.5	1158	4	US-10-287-035-26
23	1788	62.5	1158	4	US-10-282-162-26
24	1788	62.5	1158	6	US-11-134-114-26
25	1783	62.3	1168	3	US-09-313-942-24
26	1783	62.3	1168	3	US-09-935-868-24
27	1783	62.3	1168	4	US-10-287-035-24

28	1783	62.3	1168	4	US-10-282-162-24	Sequence 24, Appl
29	1783	62.3	1168	6	US-11-134-114-24	Sequence 24, Appl
30	1683	58.8	315	3	US-09-313-942-16	Sequence 16, Appl
31	1683	58.8	315	3	US-09-935-868-16	Sequence 16, Appl
32	1683	58.8	315	4	US-10-287-035-16	Sequence 16, Appl
33	1683	58.8	315	4	US-10-282-162-16	Sequence 16, Appl
34	1683	58.8	315	6	US-11-134-114-16	Sequence 16, Appl
35	954.5	33.4	387	4	US-10-322-696-141	Sequence 141, Appl
36	954.5	33.4	460	4	US-10-247-463-13	Sequence 13, Appl
37	954.5	33.4	460	6	US-11-016-106-13	Sequence 13, Appl
38	939.5	32.8	266	6	US-11-043-788-194	Sequence 194, Appl
39	938.5	32.8	212	3	US-09-854-280-14	Sequence 14, Appl
40	938.5	32.8	212	3	US-09-854-208-14	Sequence 14, Appl
41	938.5	32.8	212	4	US-10-099-007A-3	Sequence 3, Appl
42	938.5	32.8	212	4	US-10-400-377-13	Sequence 13, Appl
43	938.5	32.8	212	4	US-10-400-708-13	Sequence 13, Appl
44	938.5	32.8	212	4	US-10-298-148-13	Sequence 13, Appl
45	938.5	32.8	212	4	US-10-440-464-61	Sequence 61, Appl

## ALIGNMENTS

RESULT 1  
US-10-485-545A-14  
; Sequence 14, Application US/10485545A  
; Publication No. US20050064558A1  
; GENERAL INFORMATION:  
; APPLICANT: University College Cardiff  
; APPLICANT: University of Wales College of Medicine  
; TITLE OF INVENTION: A Fusion Protein  
; FILE REFERENCE: P102803PCT  
; CURRENT APPLICATION NUMBER: US/10/485,545A  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: 0119015.6  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Seqwin99, version 1.02  
; SEQ ID NO 14  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-6 fusion protein  
US-10-485-545A-14

Query Match		96.9%	Score 2772;	DB 5;	Length 569;
Best Local Similarity		95.4%	Pred. No. 2.2e-206;		
Matches 535;		Conservative 0;	Mismatches 6;	Indels 20;	Gaps 3;
QY	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTTLT	CPGVEPEDNATVHW	60	
DB	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTTLT	CPGVEPEDNATVHW	60	
QY	61	VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGT	VHLLVDVPPPEPQLS	120	
DB	61	VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGT	VHLLVDVPPPEPQLS	120	
QY	121	CFRKPSPLNVCEWGPSTPSLT	TKAVLLVRKFSQSPAE	180	
DB	121	CFRKPSPLNVCEWGPSTPSLT	TKAVLLVRKFSQSPAE	180	
QY	181	PGDSSFFYIVSMCVASSVSGSKFTQT	FOGCGILOPPANTITVTAVARNPRLWSVTWOD	240	
DB	181	PGDSSFFYIVSMCVASSVSGSKFTQT	FOGCGILOPPANTITVTAVARNPRLWSVTWOD	240	
QY	241	PHSMNSSFYRLRFELRYAERSKTFT	TMWKDLQHCVTHDAWSGLRHVVQLRAQEFQ	300	
DB	241	PHSMNSSFYRLRFELRYAERSKTFT	TMWKDLQHCVTHDAWSGLRHVVQLRAQEFQ	300	
QY	301	GWSEWSPEAMGTPWTESRPPAE	NEVSTPMQALTTNKDDNILLFRDSANATSLP	355	
DB	301	GWSEWSPEAMGTPWTESRPPAE	NEVSTPMQALTTNKDDNILLFRDSANATSLP	355	

Qy 356 -----VEFMPVPPGDSKOVAAHROPLTSSRIDKQIRYILDGIALRKET 402  
Db 361 GSCGLGGGGGGSLFPFGEDSKOVAAHROPLTSSRIDKQIRYILDGISA-RKET 419  
Qy 403 CNKSNMCESSKEALAEENLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLN 462  
Db 420 CNKSNMCESSKEALAEENLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLN 479  
Qy 463 RFESSEEQARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQONQWLODMTT 522  
Db 480 RFESSEEQARAVOMSTKVLIOF-QKAKNLDAITTPDPTTNASLLTKLQONQWLODMTT 538  
Qy 523 HLILRSKFELQSSLRALQOM 543  
Db 539 HLILRSKFELQSSLRALQOM 559

RESULT 2  
US-09-313-942-8  
; Sequence 8, Application US/09313942  
; Publication No. US20020012962A1  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-8

Query Match 67.1%; Score 1921; DB 3; Length 592;  
Best Local Similarity 77.1%; Pred. No. 3.1e-140;  
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MVAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOLS 120  
Db 61 VLRKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQKSFSCOLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQKSFSCOLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNPRLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNPRLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEEFGQ 300  
Qy 301 GEWSEWPEAMGTPTWESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360  
Db 301 GEWSEWPEAMGTPTWESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360  
Qy 361 VPPGEDSKOVAAHROPLTSSRIDKQIRYILDGIALRKETCNKNMCE--SSKEALAE 418  
Db 358 -----DAGEP-----KSCDKTHTCPPCAPPELLGG 382

RESULT 4  
US-10-287-035-8  
; Sequence 8, Application US/10287035

Qy 419 NNLNLPKMAEKDGCFCQSGFNEETCLVKIIT---GLLEFEVYLEYQ---NRFESSEEQAR 472  
Db 383 PSVFLFPFKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYN 442  
Qy 473 AVQMSTKVL 481  
Db 443 STYRVVSVL 451

RESULT 3  
US-09-935-868-8  
; Sequence 8, Application US/09935868  
; Patent No. US20020164690A1  
; GENERAL INFORMATION:  
; APPLICANT: Regeneron Pharmaceuticals, Inc  
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
; FILE REFERENCE: REG 203D  
; CURRENT APPLICATION NUMBER: US/09/935,868  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-868-8

Query Match 67.1%; Score 1921; DB 3; Length 592;  
Best Local Similarity 77.1%; Pred. No. 3.1e-140;  
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MVAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOLS 120  
Db 61 VLRKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQKSFSCOLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYQSQKSFSCOLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNPRLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNPRLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEEFGQ 300  
Qy 301 GEWSEWPEAMGTPTWESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360  
Db 301 GEWSEWPEAMGTPTWESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360  
Qy 361 VPPGEDSKOVAAHROPLTSSRIDKQIRYILDGIALRKETCNKNMCE--SSKEALAE 418  
Db 358 -----DAGEP-----KSCDKTHTCPPCAPPELLGG 382

RESULT 4  
US-10-287-035-8  
; Sequence 8, Application US/10287035





Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPABDFQPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
QY 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360  
Db 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360  
QY 361 VPPGEDSKDVAAP 373  
Db 357 ----QDSSSVPLP 365

RESULT 9  
US-11-016-106-12  
; Sequence 12, Application US/11016106  
; Publication No. US20050106673A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Lynette M.  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: DX09920  
; CURRENT APPLICATION NUMBER: US/11/016,106  
; PRIOR FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: primate  
US-11-016-106-12

Query Match 67.0%; Score 1918; DB 6; Length 468;  
Best Local Similarity 96.5%; Pred. No. 3.8e-140;  
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPABDFQPCQYSESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPABDFQPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
QY 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360  
Db 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

QY 361 VPPGEDSKDVAAP 373  
Db 357 ----QDSSSVPLP 365

RESULT 10  
US-09-313-942-15  
; Sequence 15, Application US/0931313942  
; Publication No. US20020012962A1  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 3; Length 360;  
Best Local Similarity 99.4%; Pred. No. 1.1e-139;  
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60  
QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPABDFQPCQYSESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPABDFQPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGILOPDPANITVTAVARNPRLSVTWOD 240  
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQBEFGQ 300  
QY 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357  
Db 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 11  
US-09-935-868-15  
; Sequence 15, Application US/09935868  
; Patent No. US20020164690A1  
; GENERAL INFORMATION:  
; APPLICANT: Regeneron Pharmaceuticals, Inc  
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
; FILE REFERENCE: REG 203D  
; CURRENT APPLICATION NUMBER: US/09/935,868  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 360

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match          66.8%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300
Db 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300

Qy 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 12
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: NEIL STAHL AND GEORGE D. YANCOPOULOS
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match          66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match          66.8%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300
Db 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300

Qy 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 13
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-15

Query Match          66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALAAAPGAAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300
Db 241 PHSWNSSFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFQG 300

Qy 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPFAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 14
US-11-134-114-15
; Sequence 15, Application US/11134114
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; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-15

Query Match      66.8%; Score 1910; DB 6; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60

Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120
Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120

Qy 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSEQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSEQSKFSCQLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300

Qy 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNLLFRDSANATSLPVE 357
Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNLLFRDSANATSLPVE 357
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RESULT 15
US-10-485-545A-11
; Sequence 11, Application US/10485545A
; Publication No. US20050064558A1
; GENERAL INFORMATION:
; APPLICANT: University College Cardiff
; APPLICANT: University of Wales College of Medicine
; TITLE OF INVENTION: A Fusion Protein
; FILE REFERENCE: P102803PCT
; CURRENT APPLICATION NUMBER: US/10/485,545A
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: 0119015.6
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 468
; TYPE: PRT
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; ORGANISM: homo sapien
US-10-485-545A-11

Query Match      66.5%; Score 1902; DB 5; Length 468;
Best Local Similarity 96.0%; Pred. No. 6.7e-139;
Matches 358; Conservative 1; Mismatches 6; Indels 8; Gaps 1;

Qy 14 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60

Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120
Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120

Qy 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSEQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFQPCQYSEQSKFSCQLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300

Qy 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNLLFRDSANATSLPVE 360
Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNLLFRDSANATSLPVE 360

Qy 361 VPPGEDSKDVAAP 373
Db 357 ----QDSSSVPLP 365
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Search completed: September 7, 2006, 23:34:34  
Job time : 182 secs

Handwritten text, possibly a signature or date, oriented diagonally.



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:31:41 ; Search time 34 Seconds  
(without alignments)  
1121.930 Million cell updates/sec

Title: US-09-462-416A-7  
Perfect score: 2861  
Sequence: 1 MLAVGCCALLAALAPGAAL.....LILRSFKFLOSSLRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1872	65.4	464	6	US-10-669-920-1407	Sequence 1407, Ap
2	938.5	32.8	212	6	US-10-505-928-453	Sequence 453, App
3	938.5	32.8	212	6	US-10-511-937-2489	Sequence 2489, Ap
4	938.5	32.8	212	6	US-10-933-854-11	Sequence 11, Appl
5	927	32.4	183	7	US-11-330-917-198	Sequence 198, App
6	913.5	31.9	454	6	US-10-669-920-1402	Sequence 1402, Ap
7	908	31.7	277	6	US-10-669-920-1405	Sequence 1405, Ap
8	303	10.6	368	6	US-10-449-902-38075	Sequence 38075, A
9	201	7.0	422	7	US-11-296-092-32	Sequence 32, Appl
10	201	7.0	422	7	US-11-296-155-32	Sequence 32, Appl
11	201	7.0	422	7	US-11-300-928-27	Sequence 27, Appl
12	198.5	6.9	328	7	US-11-234-676-4	Sequence 4, Appl
13	167.5	5.9	918	7	US-11-275-181-6	Sequence 6, Appl
14	158.5	5.5	335	7	US-11-234-676-321	Sequence 321, App
15	155	5.4	306	6	US-10-669-920-93	Sequence 8, Appl
16	155	5.4	604	6	US-10-669-920-95	Sequence 95, Appl
17	146	5.1	890	6	US-10-553-520-180	Sequence 180, App
18	140.5	4.9	347	6	US-10-669-920-108	Sequence 108, App
19	139	4.9	229	7	US-11-297-134-8	Sequence 8, Appl
20	139	4.9	229	7	US-11-275-181-5	Sequence 5, Appl
21	138	4.8	268	6	US-10-669-920-104	Sequence 104, App
22	138	4.8	374	6	US-10-669-920-102	Sequence 102, App
23	138	4.8	618	6	US-10-669-920-110	Sequence 110, App
24	131.5	4.6	324	7	US-11-353-451-10	Sequence 10, Appl
25	131.5	4.6	519	7	US-11-301-764-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

US-10-669-920-1407  
; Sequence 1407, Application US/10669920  
; Publication No. US20060194265A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
; FILE REFERENCE: 20366-066001  
; CURRENT APPLICATION NUMBER: US/10/669,920  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: US 10/004,113  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 10/052,482  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/997,722  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 10/034,650  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 10/085,117  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 10/087,192  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 10/322,281  
; PRIOR FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US 10/322,696  
; PRIOR FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 1441  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1407  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-669-920-1407

Query Match 65.4%; Score 1872; DB 6; Length 464;

Best Local Similarity 95.2%; Pred. NO. 1.3e-129;

Matches 355; Conservative 1; Mismatches 5; Indels 12; Gaps 3;

QY 1 MLAVGCCALLAALAPGAALAPRRCPAEGVLTSLPGDSVTLTCGVEPEDNATVHW 60

DB 1 MLAVGCCALLAALAPGA--APRRCPAQEV--VLTSLPGDSVTLTCGVEPEDNATVHW 56

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRAGTGVHLLVDVPPPEPQLS 120

DB 57 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRAGTGVHLLVDVPPPEPQLS 116

QY 121 CFRKSPLSNVVCEWNGPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSQQLAV 180

|||||  
Db 117 CFRKSPLSNVCEWGPSTPSLTTKAVLLVRKFNQSPADFEQPCQXSQESQKSCQAV 176  
|||||  
Qy 181 PEGDSFFIVSMCVASSVSGSKFTQTTFQGGGILQDPDPANITVTAVARNRWLSVTWQD 240  
|||||  
Db 177 PEGDSFFIVSMCVASSVSGSKFTQTTFQGGGILQDPDPANITVTAVARNRWLSVTWQD 236  
|||||  
Qy 241 PHSWNSSRYRFLRYRAERSKFTTMMVKDLQHCCHVHDWAGSLRHVVQLRAQEBFGQ 300  
|||||  
Db 237 PHSWNSSRYRFLRYRAERSKFTTMMVKDLQHCCHVHDWAGSLRHVVQLRAQEBFGQ 296  
|||||  
Qy 301 GEWSEWSPGATPWTESRSPAEENVSTPMQALTTNKDDNLLFRSANATSLPVEFMP 360  
|||||  
Db 297 GEWSEWSPGATPWTESRSPAEENVSTPMQALTTNKDDNLLFRSANATSLPV---- 352  
|||||  
Qy 361 VPPGEDSKDVAAP 373  
|||  
Db 353 ----QDSSSVPLP 361

RESULT 2  
US-10-505-928-453  
; Sequence 453, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 453  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-453

Query Match 32.8%; Score 938.5; DB 6; Length 212;  
Best Local Similarity 97.9%; Pred. No. 1.5e-61;  
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
Qy 354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412  
Db 22 LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81  
  
Qy 413 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQAR 472  
Db 82 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQAR 141  
  
Qy 473 AVQMTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLILRSPKEF 532  
Db 142 AVQMTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLILRSPKEF 201  
  
Qy 533 LQSSLRALROM 543  
Db 202 LQSSLRALROM 212

RESULT 3  
US-10-511-937-2489  
; Sequence 2489, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald

4  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2489  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2489

Query Match 32.8%; Score 938.5; DB 6; Length 212;  
Best Local Similarity 97.9%; Pred. No. 1.5e-61;  
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
Qy 354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412  
Db 22 LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81  
  
Qy 413 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQAR 472  
Db 82 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQAR 141  
  
Qy 473 AVQMTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLILRSPKEF 532  
Db 142 AVQMTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLILRSPKEF 201  
  
Qy 533 LQSSLRALROM 543  
Db 202 LQSSLRALROM 212

RESULT 4  
US-10-933-854-11  
; Sequence 11, Application US/10933854  
; Publication No. US20060105347A1  
; GENERAL INFORMATION:  
; APPLICANT: GTC Biotherapeutics, Inc.  
; APPLICANT: Meade, Harry  
; APPLICANT: Cox, Geoffrey F.  
; TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammals  
; FILE REFERENCE: GTC-220 PCT  
; CURRENT APPLICATION NUMBER: US/10/933,854  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 60/500,910  
; PRIOR FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Human a Interferon Variant 2A  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank/EMBL/DBJ Accession No. CAA00839  
; DATABASE ENTRY DATE: 1993-12-03  
; RELEVANT RESIDUES: (1)..(212)  
US-10-933-854-11

Query Match 32.8%; Score 938.5; DB 6; Length 212;  
Best Local Similarity 97.9%; Pred. No. 1.5e-61;

Matches	187;	Conservative	0;	Mismatches	3;	Indels	1;	Gaps	1
Qy	354	LPVVF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKNMCSS	412						
Db	22	LPAAPFAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKNMCSS	81						
Qy	413	KEALAEKNLNLPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVLYEVLONPESSEQAR	472						
Db	82	KEALAEKNLNLPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVLYEVLONPESSEQAR	141						
Qy	473	AVQMSKTVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLODMTTHILRSPKEF	532						
Db	142	AVQMSKTVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLODMTTHILRSPKEF	201						
Qy	533	LOSSLRALRQW	543						
Db	202	LOSSLRALRQW	212						

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RESULT 5
US-11-330-917-198
; Sequence 198, Application US/11330917
; Publication No. US20060182716A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Jin
; APPLICANT: Seiwert, Scott D.
; APPLICANT: Blatt, Lawrence M.
; TITLE OF INVENTION: Synthetic Hyperglycosylated, Protease-Resistant Polypeptide Variants
; TITLE OF INVENTION: Oral Formulations and Methods of Using the Same
; FILE REFERENCE: INTM-060W0
; CURRENT APPLICATION NUMBER: US/11/330,917
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 60/600,202
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/600,134
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/604,280
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/604,415
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 1354
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-330-917-198

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RESULT 6  
US-10-669-920-1402  
; Sequence 1402, Application US/10669920  
; Publication No. US20060194265A1

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; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1402
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-1402

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RESULT 7  
US-10-669-920-1405  
; Sequence 1405, Application US/10669920  
; Publication No. US20060194265A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Malandro, Marc S.  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
; FILE REFERENCE: 20366-066001

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; CURRENT APPLICATION NUMBER: US/10/569,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-669-920-1405

Query Match      31.7%; Score 908; DB 6; Length 277;
Best Local Similarity 92.9%; Pred. No. 3.6e-59;
Matches 169; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 192 MCVASSVGSFKSKTQTGGCIGILOPPANITVTAVARNPRLSVTWQDPHSMNSFYRL 251
Db 1 MCVASSVGSFKSKTQTGGCIGILOPPANITVTAVARNPRLSVTWQDPHSMNSFYRL 60

Qy 252 RFELRYRAERSKTFTHVMVKDQHCVTHDAWSGLRHVVQLRAQEEFGQGEWSPEAM 311
Db 61 RFELRYRAERSKTFTHVMVKDQHCVTHDAWSGLRHVVQLRAQEEFGQGEWSPEAM 120

Qy 312 GTPWTSRSPPAENEVSTPMQALTNKDDNLLFRDSANATSLPVEFMPVPVPGDSDKVA 371
Db 121 GTPWTSRSPPAENEVSTPMQALTNKDDNLLFRDSANATSLPVEFMPVPVPGDSDKVA 172

Qy 372 AP 373
Db 173 LP 174

RESULT 8
US-10-449-902-38075
; Sequence 38075, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38075
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-38075

Query Match      10.6%; Score 303; DB 6; Length 368;

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Best Local Similarity 28.4%; Pred. No. 1.3e-14;
Matches 108; Conservative 44; Mismatches 148; Indels 80; Gaps 17;

Qy 12 LLAAPGAALAPRCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWLRLKPAAGSHP 71
Db 12 LLAAGVVAYAQRH---SQDTHVLYERLGSVDVILPC-GTAAWGTAVTWVNGTDLAAHY 67

Qy 72 SRWAGMRLLRLRSVQLHDSGNYSCYRAG---RPAGTVHLLVDPPEEPQLSCFRKSPL 127
Db 68 N-----GSQVLVEGLDLSHSGHVACVQSSWHLRYQALLH--VGMPPREPVLTCRSNSYP 120

Qy 128 SNVVCW---GPRSTPSLITKAVLLVRKP---QNSPAEDFQEPQCISQESQKSCQLAVP 181
Db 121 KGFYCSWHLSPSTFIPTNFVTVLHGSKLLGCKDPA-----PKNRCHIRYT 167

Qy 182 EGDSSF-YIVSMCVASSVGSFKSKTQTFQCGCIGILOPPANITVTAVARNPRLSVTWQD 240
Db 168 HLFSTVKYKVTLVTNALGHN-STAITFDEFTIVKPDPPENVVAVRPPVSPRRLLEVWQT 226

Qy 241 PHSW-NSSFYRLRFELRYRAERSKTFTHVMVKDQHC-----VIHDAWSGLRHVVQ 291
Db 227 PSSWPDPESPPLKFFLYRP-----LILDQWQHVELSDGTTHTITDAYAGKEYIIQ 277

Qy 292 LRAQEEFGQGEWSPEAMGTPTESRSPPAENEVSTPMQALTNKDDNLLFRDSANA 351
Db 278 VAAKDN-EIGTWSDSVVAHAHATPTEE-----PRYLTTEAQAPET-----T 317

Qy 352 TSLPVEFMPVP-----PGE 365
Db 318 TTTTTSFVPPPTTKICDPGE 337

RESULT 9
US-11-296-092-32
; Sequence 32, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

```

```
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-296-092-32

Query Match          7.0%; Score 201; DB 7; Length 422;
Best Local Similarity 24.7%; Pred. No. 4.6e-07;
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

QY 8 LLAALLAAGA-----ALAPRCFAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWV 61
DB 24 LLLCVLGAPRAGSGAHTAVISQDP-----TLIGSSLLATC-----SVHG- 64
QY 62 LRKPAAGSHPSRWAGMGRLL-----LLRSVQLHDSGNYSCY-RAGRP 102
DB 65 -DPPGATAEGLYWTNGRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSI 123
QY 103 AGTVHLLVDVPEEP-QLSCFRKSPLSNVVCEWGP-----RSTPSLTTKAVLLVRKF 153
DB 124 LAGSCLYVGLPEKPVNISCSKN-MKDLTCWTGAGHGETFLHTNYSLYK-----LRWY 178
QY 154 -QNSPAEDFQBPQCOYSQBSQKFSQCLAVPEGDSSF--YIVSMCVASSVSGSKFTQTQFG 210
DB 179 QDNTCEYHTVGPH-----SCH--IPKDLALFTPYEIVWEATNRLGSARSDVLTLDI 229
QY 211 CGILOPDPANITVTAVARNPRWLSVTWQDPHSWNSSPYRLRFELRYAERSKFTTMMV 270
DB 230 LDVVTDDPPDVHVSRRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDS---VDWKV 286
QY 271 KD---LQHCVTHDAWSGLRHVVQLRAQEEFG-----QGEWSEWS-PEAMGTPWTESRS 320
DB 287 VDDVSNQTSCLAGLKPGTVFVQVRC-NPFGIYSGKAGIWESEHPTAASTPRSRPG 345
QY 321 P-----PAENEVSTPMQALTNNKDDNILFR 346
DB 346 FGGACEPRGSGPVRRELKQFLGWLKKHAYCSNLSFR 386

RESULT 10
US-11-296-155-32
; Sequence 32, Application US/11296155
; Publication No. US20060127983A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/11/296,155
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/09/866,028
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-296-155-32

Query Match          7.0%; Score 201; DB 7; Length 422;
Best Local Similarity 24.7%; Pred. No. 4.6e-07;
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

QY 8 LLAALLAAGA-----ALAPRCFAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWV 61
DB 24 LLLCVLGAPRAGSGAHTAVISQDP-----TLIGSSLLATC-----SVHG- 64
QY 62 LRKPAAGSHPSRWAGMGRLL-----LLRSVQLHDSGNYSCY-RAGRP 102
DB 65 -DPPGATAEGLYWTNGRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSI 123
QY 103 AGTVHLLVDVPEEP-QLSCFRKSPLSNVVCEWGP-----RSTPSLTTKAVLLVRKF 153
DB 124 LAGSCLYVGLPEKPVNISCSKN-MKDLTCWTGAGHGETFLHTNYSLYK-----LRWY 178
QY 154 -QNSPAEDFQBPQCOYSQBSQKFSQCLAVPEGDSSF--YIVSMCVASSVSGSKFTQTQFG 210
DB 179 QDNTCEYHTVGPH-----SCH--IPKDLALFTPYEIVWEATNRLGSARSDVLTLDI 229
QY 211 CGILOPDPANITVTAVARNPRWLSVTWQDPHSWNSSPYRLRFELRYAERSKFTTMMV 270
DB 230 LDVVTDDPPDVHVSRRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDS---VDWKV 286
QY 271 KD---LQHCVTHDAWSGLRHVVQLRAQEEFG-----QGEWSEWS-PEAMGTPWTESRS 320
DB 287 VDDVSNQTSCLAGLKPGTVFVQVRC-NPFGIYSGKAGIWESEHPTAASTPRSRPG 345
QY 321 P-----PAENEVSTPMQALTNNKDDNILFR 346
DB 346 FGGACEPRGSGPVRRELKQFLGWLKKHAYCSNLSFR 386

RESULT 11
US-11-300-928-27
; Sequence 27, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
; APPLICANT: Karumanchi, S. Ananth
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treati
; TITLE OF INVENTION: Complications of Pregnancy
; FILE REFERENCE: 01948/108002
; CURRENT APPLICATION NUMBER: US/11/300,928
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US 60/636,275
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QY 325 NE-----VSTPMQA-----LITNKDD----- 341  
 Db 341 TQGYRTVOLWKTLPPEFANGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTDYRYLATL 400  
 QY 342 ---NLFRDSANATSLPV-EMWPPPGEDSKDVAAPHQPL-----TSSERIDKQIRYIL 392  
 Db 401 TVRLNVGKSDAAVITPACDFQATHPVMDLK--APPKONMLWVETTPRESVKK---YIL 455  
 QY 393 DGISALRKETC 403  
 Db 456 EMCVLSDKAPC 466

RESULT 14  
 US-11-234-676-321  
 ; Sequence 321, Application US/11234676  
 ; Publication No. US20060193821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cload, Sharon T.  
 ; APPLICANT: Diener, John L.  
 ; APPLICANT: Ferguson, Alicia  
 ; APPLICANT: Hamaguchi, Nobuko  
 ; APPLICANT: Keene, Sara C.  
 ; APPLICANT: Lagasse, H.A. Daniel  
 ; APPLICANT: Sawhney, Pooja  
 ; APPLICANT: Thompson, Kristin  
 ; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as  
 ; TITLE OF INVENTION: Autoimmune Disease Therapeutics  
 ; FILE REFERENCE: 23239-578 CIP  
 ; CURRENT APPLICATION NUMBER: US/11/234,676  
 ; CURRENT FILING DATE: 2005-09-22  
 ; PRIOR APPLICATION NUMBER: 11/075,649  
 ; PRIOR FILING DATE: 2005-03-07  
 ; PRIOR APPLICATION NUMBER: 60/550,962  
 ; PRIOR FILING DATE: 2004-03-05  
 ; PRIOR APPLICATION NUMBER: 60/608,046  
 ; PRIOR FILING DATE: 2004-09-07  
 ; NUMBER OF SEQ ID NOS: 323  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 321  
 ; LENGTH: 335  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-234-676-321

Query Match 5.5%; Score 158.5; DB 7; Length 335;  
 Best Local Similarity 21.1%; Pred. No. 0.00044;  
 Matches 68; Conservative 51; Mismatches 113; Indels 91; Gaps 15;  
 QY 39 PGDSVTLTCGVEPEDNATVHW--LRKPAAGSHPSRWAGMGRLLRLRSVOLHDSGNYS 96  
 Db 42 PGETVNLTCDTPEEDD---ITWTSQRHGVIGS-----GKLTITVKEFLDAGQYTC 90  
 QY 97 YRAGRPAGTVHLLVDVP-----PEEPOLSCFRKSPLSNVVCEW----- 134  
 Db 91 HKGETLSHLLHKKENGIGWSTILKNFKNFKLCEAPNYSGRFTCSMLVQRNMDLK 150  
 QY 135 ---GPRSTP-----SLTTKAVLLVRKFNQSPAEQPCQYQSEKQSCQ--L 178  
 Db 151 FNRIKSSSSPSDRAVTCGMSILSAEKVTL-----DORDYEKYSVSCQEDV 195  
 QY 179 AVPEGDSFYIVSMCVASSVSGSKFSTOT-FQCGGILQDPDP--VTAVARNPRLSVT 237  
 Db 196 TCPTAEETLPI-ELALEARQONKYNYSFPIRDIIRKPPKQLQMKPLKNSQ--VEVS 252  
 QY 238 WODPHSMNS--SFYRLRFLRYRAERSKTFITTMVKDLQHHCVIHDW----- 284  
 Db 253 WEYPDSTPHSYFSLKFFVRIQRKEK-----MKETECCNQKGAFLVEKTSVEVQCK 306  
 QY 285 GLRHVVQLRAQEEFGCGEWSPE 307  
 Db 307 GGNVCVQ--AQDRYNNSSCSKWA 327

RESULT 15  
 US-10-669-920-93  
 ; Sequence 93, Application US/10669920  
 ; Publication No. US20060194265A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; APPLICANT: Malandro, Marc S.  
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
 ; FILE REFERENCE: 20366-066001  
 ; CURRENT APPLICATION NUMBER: US/10/669,920  
 ; CURRENT FILING DATE: 2003-09-23  
 ; PRIOR APPLICATION NUMBER: US 10/004,113  
 ; PRIOR FILING DATE: 2001-10-23  
 ; PRIOR APPLICATION NUMBER: US 10/052,482  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/997,722  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: US 10/034,650  
 ; PRIOR FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: US 10/085,117  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: US 10/087,192  
 ; PRIOR FILING DATE: 2002-03-01  
 ; PRIOR APPLICATION NUMBER: US 10/322,281  
 ; PRIOR FILING DATE: 2002-12-17  
 ; PRIOR APPLICATION NUMBER: US 10/322,696  
 ; PRIOR FILING DATE: 2002-12-17  
 ; NUMBER OF SEQ ID NOS: 1441  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 93  
 ; LENGTH: 306  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-669-920-93

Query Match 5.4%; Score 155; DB 6; Length 306;  
 Best Local Similarity 22.6%; Pred. No. 0.00071;  
 Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;  
 QY 113 PPEPQLSCFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFNQSPAEQPCQYQSESQ 172  
 Db 20 PPGKPEITHKCRSPDKETFTTCWNPGRSGGLPTNYSL-----TYSKEGE 62  
 QY 173 K--FSCQLAVPEGDSS-----FYIVSMCVASSVSGSKFSTOTFQCGGILQDPDP 218  
 Db 63 KNTYECDDYKTSGNPSCFFSKQYTSIWKIYIITVNATNEMSGSTSDPLYVDVYIIVEPEP 122  
 QY 219<sup>a</sup>PANIT--VTAVARNPRLSVTWQDP--HSMNSSFYRLRFLRYRAERSKTFITTMVKDLQ 274  
 Db 123 PRNLTLEVQKLDKKTLYLWVKWLPPTITDVKTGWFTMEYIRLKSEEA---DEWEIHFTG 179  
 QY 275 HHC--VHDAWGLRHVVQLRAQEEFGCGEWSPE 309  
 Db 180 HQTOFKVPDLVPGQKLYQVTRCKPD--HGYWSRMQGE 214

Search completed: September 7, 2006, 23:35:13  
 Job time : 35 secs

1. 1991-1992



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 22:54:31 ; Search time 193 Seconds  
(without alignments)  
1310.055 Million cell updates/sec

Title: US-09-462-416a-13

Perfect score: 2912  
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILSRKPEFLQSSLRALRQM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2846	97.7	543	2	AA03164 Chimeric
2	2786.5	95.7	570	6	ABP72702 Human int
3	2661	91.4	525	2	AAW36846 Human fus
4	2658.5	91.3	515	3	AAAB15404 IL-6R/IL-
5	2527.5	86.8	500	2	AAW36847 Human fus
6	2144.5	73.6	419	2	AAW30938 Human IL-
7	1929	66.2	690	3	AAW92195 Human IL-
8	1927.5	66.2	592	2	AAW70797 Human int
9	1927.5	66.2	592	3	AAW92185 Human IL-
10	1927.5	66.2	592	7	ABW02165 Human IL-
11	1923.5	66.1	468	3	AAW92196 Human IL-
12	1922	66.0	477	3	AAW92197 Human IL-
13	1917	65.8	468	1	AAW90284 Sequence
14	1917	65.8	468	2	AAW92195 IL-6 rece
15	1917	65.8	468	4	AAW36655 Human IL-
16	1917	65.8	468	5	AAW28593 Interleuk
17	1917	65.8	468	5	ABB78191 Amino aci
18	1917	65.8	468	6	ABP72697 Human int
19	1917	65.8	468	7	ADC07187 Human int
20	1917	65.8	468	8	ADP54591 Human PRO
21	1917	65.8	468	8	ADP23941 PRO polyp
22	1917	65.8	468	9	ADZ13887 Human can
23	1917	65.8	468	9	ADZ25538 Human IL-

24	1917	65.8	468	9	ADZ65022 Human IL-
25	1917	65.8	468	9	AED08341 Amino aci
26	1917	65.8	468	9	AED96935 Human C-r
27	1914	65.7	365	9	AED65387 Human int
28	1914	65.7	468	2	AAW98364 Interleuk
29	1913	65.7	357	6	ABP72699 Soluble i
30	1910	65.6	360	2	AAW70804 Amino aci
31	1910	65.6	360	3	AAW92199 Soluble h
32	1910	65.6	360	7	ABW02172 Human IL-
33	1909	65.6	468	1	AAW90525 B cell st
34	1907	65.5	364	6	ABP72698 Soluble i
35	1899	65.2	468	2	AAW71371 Human int
36	1891.5	65.0	499	9	AED96936 Human C-r
37	1858	63.8	345	3	AAW55071 SR345 pro
38	1852	63.6	344	1	AAW90528 B cell st
39	1822.5	62.6	453	8	ADQ59508 Human can
40	1791	61.5	384	9	AED96937 Human C-r
41	1789	61.4	1158	3	AAW92205 Fusion po
42	1789	61.4	1158	7	ABW02178 Human cyt
43	1783	61.2	1168	3	AAW92204 Fusion po
44	1783	61.2	1168	7	ABW02177 Human cyt
45	1764	60.6	1042	2	AAW70122 IL8-R typ

#### ALIGNMENTS

##### RESULT 1

AA03164	ID	AA03164	standard; protein; 543 AA.
XX	AC	AA03164;	
XX	DT	11-JUN-1999	(first entry)
XX	DE	Chimeric sIL-6R/IL-6 protein.	
XX	KW	Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;	
KW	KW	chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;	
KW	KW	highly malignant cancer cell; in vivo engraftment; mammalian cancer;	
KW	KW	human haematopoietic cell; bone marrow transplantation; mammalian cancer;	
KW	KW	hepatotoxic agent protection; haematopoiesis; liver disorder;	
XX	OS	neurological disorder.	
XX	OS	Synthetic.	
XX	FN	WO9902552-A2.	
XX	PD	21-JAN-1999.	
XX	PF	09-JUL-1998; 98WO-IL000321.	
XX	PR	10-JUL-1997; 97IL-00121284.	
XX	PR	30-DEC-1997; 97IL-00122818.	
XX	PA	(YEDA ) YEDA RES & DEV CO LTD.	
XX	PI	Revel M, Chebath J, Lapidot T, Kollet O;	
XX	DR	WPI; 1999-120776/10.	
XX	PT	New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.	
XX	PT	treating cancers, bone marrow transplantation, increasing haematopoiesis	
XX	PS	or treating liver or neurological disorders.	
XX	XX	Claim 6; Fig 3; 77pp; English.	
XX	CC	This sequence represents the chimeric glycosylated soluble interleukin-6	
XX	CC	receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the	
XX	CC	invention. It comprises a fusion protein product between all of the	
XX	CC	naturally occurring form of sIL-6R and all of the naturally occurring	
XX	CC	form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a	
XX	CC	similar fashion to the glycosylation of naturally occurring sIL-6R and IL	

CC -6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of  
 CC highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo  
 CC engraftment of human haematopoietic cells in bone marrow transplantation  
 CC and protecting liver from hepatotoxic agents. They can be used for the  
 CC preparation of a medicament for treating mammalian cancers by way of  
 CC inhibition of cancer cells, for enhancement of bone marrow  
 CC transplantation by way of eliciting engraftment of human haematopoietic  
 CC cells in bone marrow transplantation, for increasing haematopoiesis, for  
 CC treating liver or neurological disorders, or in other applications in  
 CC which IL-6 or sIL-6R are used  
 XX  
 XX  
 SQ Sequence 543 AA;

Query Match 97.7%; Score 2846; DB 2; Length 543;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-187;  
 Matches 543; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
 Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 Db 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGNYSCYRAGRPAGTVHLLVDVPPPEEQLS 120  
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGNYSCYRAGRPAGTVHLLVDVPPPEEQLS 120  
 Qy 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKFSQCLAV 180  
 Db 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKFSQCLAV 180  
 Qy 181 PEGDSSFFIVSMCVASSVSGSKFSTQTFQGGGILQPPPPANITVAVARNPRLSVTWQD 240  
 Db 181 PEGDSSFFIVSMCVASSVSGSKFSTQTFQGGGILQPPPPANITVAVARNPRLSVTWQD 240  
 Qy 241 PHSWNSSPYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAMSGLRHVQLRAQEEFGQ 300  
 Db 241 PHSWNSSPYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAMSGLRHVQLRAQEEFGQ 300  
 Qy 301 GESEWSEANGTWTESRSPPAENESTVTPMQALITNKDDNIIIFRDSANATSLPVFEFGA 360  
 Db 301 GESEWSEANGTWTESRSPPAENESTVTPMQALITNKDDNIIIFRDSANATSLPVFE--- 357  
 Qy 361 GLVLGGOPMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCKNSMCE 420  
 Db 358 -----FMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCKNSMCE 410  
 Qy 421 SSKEALAEENNLNPKMAEKDGCFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFESSEEQ 480  
 Db 411 SSKEALAEENNLNPKMAEKDGCFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFESSEEQ 470  
 Qy 481 ARAVQMSTKVLIQFLOKAKNLDATTPDPTTNASLTITKLOAQNQWLQDMTHILIRSPK 540  
 Db 471 ARAVQMSTKVLIQFLOKAKNLDATTPDPTTNASLTITKLOAQNQWLQDMTHILIRSPK 530  
 Qy 541 EFLOSSLRALRQM 553  
 Db 531 EFLOSSLRALRQM 543

RESULT 2  
 ABP72702  
 ID ABP72702 standard; protein; 570 AA.  
 XX  
 AC ABP72702;  
 XX  
 DT 11-JUN-2003 (first entry)  
 XX  
 DE Human interleukin-6-receptor isoform DS-sIL-6R fusion protein.  
 XX  
 KW Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;  
 KW anti-HIV; antirheumatic; antiarthritic; antiinflammatory;  
 KW immunosuppressive; gene therapy.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 XX Protein 1..364  
 FT /label= DS-sIL-6R  
 FT Peptide 365..376  
 FT /label= Linker  
 FT Protein 377..560  
 FT /label= IL-6  
 FT Peptide 561..570  
 FT /label= C-myc tag  
 XX  
 XX WO2003014359-A2.  
 XX  
 XX 20-FEB-2003.  
 XX  
 XX 02-AUG-2002; 2002WO-GB003581.  
 XX  
 XX 03-AUG-2001; 2001GB-00019015.  
 XX  
 XX (UYCA-) UNIV COLLEGE CARDIFF.  
 XX PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
 XX  
 XX Jones SA, Topley N;  
 PI  
 XX  
 XX WPI; 2003-256588/25.  
 DR  
 XX  
 XX  
 XX New fusion protein having a functional IL-6 and DS-sIL-6R molecule,  
 FT useful for the manufacture of a medicament for the prophylaxis or  
 FT treatment of an infectious disease, and an inflammatory or immunological  
 FT disorder.  
 XX  
 XX Disclosure; Fig 5; 46pp; English.  
 XX  
 XX  
 CC The present sequence is the protein sequence of a novel fusion protein  
 CC comprising a soluble form of the human interleukin-6 receptor, denoted DS  
 CC -sIL-6R (see also ABP726588), joined via a peptide linker to a human IL-6  
 CC molecule (see also ABP72700), with a C-terminal c-myc tag sequence.  
 CC Administration of this fusion protein results in the increased expression  
 CC of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. High levels of  
 CC MIP-1alpha, MIP-1beta and RANTES complete with HIV for binding to CCR5  
 CC and effectively suppress HIV entry. The fusion protein can be used in the  
 CC treatment of any disease in which the infectious agent binds to CCR5,  
 CC especially M-trophic strains of HIV. The invention also provides a  
 CC nucleic acid molecule encoding the fusion protein, an expression vector,  
 CC a host cell, and a method of producing the fusion protein in the host  
 CC cell. The fusion protein, nucleic acid or vector can be used in the  
 CC manufacture of a medicament for the prophylaxis or treatment of an  
 CC infectious disease (especially AIDS caused by a M-trophic strain of HIV,  
 CC or bacterial peritonitis), an inflammatory disorder or an immunological  
 CC disorder (especially rheumatoid arthritis), when it is desirable to  
 CC increase or resolve an immune response (claimed)  
 XX  
 XX Sequence 570 AA;  
 SQ

Query Match 95.7%; Score 2786.5; DB 6; Length 570;  
 Best Local Similarity 96.1%; Pred. No. 3.1e-183;  
 Matches 540; Conservative 0; Mismatches 11; Indels 11; Gaps 4;  
 Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 Db 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGNYSCYRAGRPAGTVHLLVDVPPPEEQLS 120  
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGNYSCYRAGRPAGTVHLLVDVPPPEEQLS 120  
 Qy 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKFSQCLAV 179  
 Db 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKFSQCLAV 179  
 Qy 180 VPEGDSSFFIVSMCVASSVSGSKFSTQTFQGGGILQPPPPANITVAVARNPRLSVTWQ 239

```
Db 180 VPEGDSFPYIVSMCVASSVSGSK-SKTQTFQCGIQLQDPPANITVTAVARNPRLSVTWQ 238
Cc 240 DPHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWSGLRHVQLRAQEEFG 299
Cc 239 DPHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWSGLRHVQLRAQEEFG 298
Cc 300 QGEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIFRDSANATSLPVE-- 357
Cc 239 QGEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIFRDSANATSLPVSRR 358
Cc 358 -----FGAGLVLGQFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 411
Cc 359 RGSCLGGGGGGGSLPEVPVPGEDSKDVAAPHROPLTSSERTDKQIRYILDGIALRKE 418
Cc 412 TCNKNMCESSKEALAEANNLNPMAEKDGCFCFSGFNEETCLVKIITGLLFEVYLEYLO 471
Cc 419 TCNKNMCESSKEALAEANNLNPMAEKDGCFCFSGFNEETCLVKIITGLLFEVYLEYLO 478
Cc 472 NRFESSEQARAVOMSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMT 531
Cc 479 NRFESSEQARAVOMSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMT 538
Cc 532 THILIRSPKFEFLOSSLRALRQM 553
Cc 539 THILIRSPKFEFLOSSLRALRQM 560

RESULT 3
AAW36846
ID AAW36846 standard; protein; 525 AA.
XX AC AAW36846;
XX DT 25-MAR-2003 (revised)
XX DT 25-MAR-1998 (first entry)
XX DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.
XX KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
XX KW protein interaction; therapeutic; antagonist.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide /label= signal_peptide
XX FT Protein /note= "H-IL-6 fusion polypeptide"
XX FT Region 324..341
XX FT /label= linker region
XX FT /note= "Links together COOH-terminus of sIL-6R with the
XX NH2-terminus of IL-6"
XX PN WO9732891-A2.
XX PD 12-SEP-1997.
XX PF 07-MAR-1997; 97WO-DE000458.
XX PR 07-MAR-1996; 96DE-01008813.
XX PA (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
XX PI Rosejohn S;
XX DR WPI: 1997-470536/43.
XX DR N-PSDB; AAT97848.
XX PT Conjugate of two peptide(s) with mutual affinity connected by a linker -
XX PT used to modulate interactions between proteins, e.g. for ex vivo
XX PT expansion of human stem cells.
```

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XX Disclosure; Fig 1; 19pp; German.
XX This sequence represents the fusion polypeptide H-IL-6 which contains an
Cc 18 amino acid linker which joins the carboxy terminus of human
Cc interleukin-6 receptor (IL-6R) with the amino terminus of human
Cc interleukin-6 (IL-6). Such conjugates could be used to modulate
Cc interactions between proteins, particularly to overcome interrupted
Cc interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
Cc constructs derived from IL-6 and its receptor, can also be used for ex
Cc vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
Cc antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
Cc MAR-2003 to correct PI field.)
XX Sequence 525 AA;

Query Match 91.4%; Score 2661; DB 2; Length 525;
Best Local Similarity 92.4%; Pred. No. 1.2e-174;
Matches 511; Conservative 1; Mismatches 13; Indels 28; Gaps 1;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEAVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
Db 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEAVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
QY 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNYSYVAGRPAGTVHLLVDVPPPEPOL 120
Db 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNYSYVAGRPAGTVHLLVDVPPPEPOL 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFPQCYSQESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFPQCYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLQDPPANITVTAVARNPRLSVTWQ 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLQDPPANITVTAVARNPRLSVTWQ 240
QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWSGLRHVQLRAQEEFG 300
Db 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWSGLRHVQLRAQEEFG 300
QY 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIFRDSANATSLPVEFGA 360
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIFRDSANATSLPVEFGA 360
QY 361 GLVLGGQFMPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKECNKNMCE 420
Db 333 GSGGGSVPEVPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKECNKNMCE 392
QY 421 SSKEALAEANNLNPMAEKDGCFCFSGFNEETCLVKIITGLLFEVYLEYQLNRFSSSEBQ 480
Db 393 SSKEALAEANNLNPMAEKDGCFCFSGFNEETCLVKIITGLLFEVYLEYQLNRFSSSEBQ 452
QY 481 ARVQMSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILIRSPK 540
Db 453 ARVQMSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILIRSPK 512
QY 541 EFLQSSLRALRQM 553
Db 513 EFLQSSLRALRQM 525

RESULT 4
AAB15404
ID AAB15404 standard; protein; 515 AA.
XX AC AAB15404;
XX DT 17-JAN-2001 (first entry)
XX DE IL-6R/IL-6 fusion protein.
XX KW Fusion protein; human; interleukin 6 receptor; Pichia pastoris; yeast;
XX KW drug; myeloid stem cell; platelet; blood.
```



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Db 1 MLAVGALLAAALAAAPGAAAPRRCPAQEVARGVLTSLFGDSVTLTCFGEVEDNATVHM 60
Qy 61 VLURKPAAGSHPSRWAGMGRLLRLRSVLQHDGNYSCYRAGRPAGTVHLLVDVPPREPOLS 120
Db 61 VLURKPAAGSHPSRWAGMGRLLRLRSVLQHDGNYSCYRAGRPAGTVHLLVDVPPREPOLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQSKFSCQLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRWLSVTWOD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRWLSVTWOD 240
Qy 241 PHSWNSSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVOLRAOEERFG 300
Db 241 PHSWNSSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVOLRAOEERFG 300
Qy 301 GEWSSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGA 360
Db 281 GEWSSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGA 360
Qy 361 GLVLGGQFMPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 420
Db 308 GSGGGGSEVPPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 367
Qy 421 SKKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVONRPFSSBEQ 480
Db 368 SKKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVONRPFSSBEQ 427
Qy 481 ARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLIRSFK 540
Db 428 ARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLIRSFK 487
Qy 541 EFLQSSLRALROM 553
Db 488 EFLQSSLRALROM 500

RESULT 6
AAV30938
ID AAV30938 standard; protein; 419 AA.
XX AC AAV30938;
XX DT 19-OCT-1999 (first entry)
XX DE Human IL-6 receptor/IL-6 fusion protein.
KW IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
KW stem cell; platelet; reduced antigenicity.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Protein 1..420
XX FT /note= "No start codon given"
XX PN JP11196867-A.
XX PD 27-JUL-1999.
XX PF 09-JAN-1998; 98JP-00002921.
XX PR 09-JAN-1998; 98JP-00002921.
XX PA (TOX) TOSOH CORP.
XX DR WPI; 1999-496648/42.
XX DR N-PSDB; AA209202.
```

```
PT New interleukin-6 receptor-interleukin-6 fused protein and gene - used
PT for growth of bone marrow stem cells and platelets.
XX
PS Example 1; Page 5-8; 8pp; Japanese.
XX
CC This invention describes a novel gene which encodes a fusion protein of
CC interleukin-6 (IL-6) receptor and bound with a gene sequence encoding for
CC IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding
CC protein has applications for the growth of bone marrow stem cells and
CC platelets. Transmision of a signal of IL-6 to target cells for
CC stimulation with reduced antigenicity is possible. This sequence
CC represents the IL-6 receptor/IL-6 fusion protein described in the
CC invention
XX
SQ Sequence 419 AA;

Query Matcha 73.6%; Score 2144.5; DB 2; Length 419;
Best Local Similarity 94.1%; Pred. No. 3.5e-139;
Matches 412; Conservative 3; Mismatches 4; Indels 19; Gaps 2;

Qy 116 EPQLSCFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQSKF 175
Db 1 EPQLSCFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQSKF 60
Qy 176 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRWLS 235
Db 61 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTQFCGILQDPDPANITVTAVARNPRWLS 120
Qy 236 VTWODPHSWNSFFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVOLRAQ 295
Db 121 VTWODPHSWNSFFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVOLRAQ 180
Qy 296 EEFQGGSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLP 355
Db 181 EEFQGGSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLP 229
Qy 356 VEFAGLVGGQFMPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNK 415
Db 230 ---SSELV---APVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNK 281
Qy 416 SNMCESKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVONRPE 475
Db 282 SNMCESKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVONRPE 341
Qy 476 SSEQARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLI 535
Db 342 SSEQARAVOMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDMTTHLI 401
Qy 536 LRSFKFELQSSLRALROM 553
Db 402 LRSFKFELQSSLRALROM 419

RESULT 7
AAV92195
ID AAV92195 standard; protein; 690 AA.
XX AC AAV92195;
XX DT 01-AUG-2000 (first entry)
XX DE Human IL-6R-alpha-C-gamma-1 fusion protein.
KW IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
KW fusion protein; cytostatic; immunomodulator; osteopathic.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 1..358
XX FT /label= IL-6R-alpha
XX FT Peptide 359..360
```

FT Protein /note= "Ala-Gly bridge"  
 FT 361.. .690  
 FT /label= C-gamma-4

PN WO200018932-A2.  
 PD 06-APR-2000.  
 XX  
 XX  
 XX  
 XX 22-SEP-1999; 99WO-US022045.  
 XX 25-SEP-1998; 98US-0101858P.  
 PR 19-MAY-1999; 99US-00313942.  
 XX (REG- ) REGENERON PHARM INC.  
 XX Stahl N, Yancopoulos GD;  
 PI WPI; 2000-293165/25.  
 DR  
 XX  
 XX Isolated nucleic acid molecule for treating cytokine-related diseases or  
 FT disorders encodes a fusion polypeptide capable of binding a cytokine to  
 FT form a nonfunctional complex.  
 XX  
 XX Example 4; Page; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that  
 CC utilizes an alpha specificity determining component, which when combined  
 CC with the cytokine, binds to a first beta signal transducing component to  
 CC form a non-functional intermediate which then binds to a second beta  
 CC signal transducing component causing beta-receptor dimerization, the  
 CC soluble alpha specificity determining component of the receptor (SK-  
 CC alpha) and the extracellular domain of the first beta signal transducing  
 CC component of the cytokine receptor (beta-1) are combined to form  
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by  
 CC binding the cytokine to form a non-functional complex. The receptor  
 CC components are shared by cytokines such as the CNF (ciliary neurotrophic  
 CC factor) family of cytokines. The invention provides the basis for the  
 CC development of IL-6 antagonists, as they show that if, in the presence of  
 CC a ligand, a non-functional intermediate complex, consisting of the  
 CC ligand, its alpha receptor and its beta-1 receptor component, can be  
 CC formed, it will effectively block the action of the ligand. Effective  
 CC antagonists of IL-6 or CNF consist of heterodimers of the extracellular  
 CC domains of the alpha specificity determining components of their  
 CC receptors and the extracellular domain of gp130. The resultant  
 CC heterodimers, function as high-affinity traps, rendering the cytokine  
 CC inaccessible to form a signal transducing complex with the native  
 CC membrane-bound forms of their receptor. The nucleic acids and  
 CC polypeptides are useful for treating cytokine-related diseases or  
 CC disorders such as osteoporosis and primary and secondary effects of  
 CC cancer including multiple myeloma or cachexia

XX  
 SQ Sequence 690 AA;

Query Match 66 2t; Score 1929; DB 3; Length 690;  
 Best Local Similarity 69.1t; Pred. No. 4.7e-124;  
 Matches 386; Conservative 29; Mismatches 66; Indels 78; Gaps 7;

Qy 1 MLAVGCALLAALLAAGPAAAPRCQAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 Db 1 MVAVGCALLAALLAAGPAAAPRCQAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGHGRLLLSVQLHDSGNYCYRAGRPAGTVHLLVDVPEEPQLS 120  
 Db 61 VLKPAAGSHPSRWAGHGRLLLSVQLHDSGNYCYRAGRPAGTVHLLVDVPEEPQLS 120

Qy 121 CFRKSPLSNVVCEGPRSTPLTAKVLLVRKFONSAPEDFOEPQYQSQSKFSCOLAV 180  
 Db 121 CFRKSPLSNVVCEGPRSTPLTAKVLLVRKFONSAPEDFOEPQYQSQSKFSCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGIILQPDPPANITVTAVARNPRLSVTWQD 240  
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGIILQPDPPANITVTAVARNPRLSVTWQD 240

4  
 Qy 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAWSGLRHVVQLRAQEBFG 300  
 Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDAWSGLRHVVQLRAQEBFG 300

Qy 301 GEWSEWSPKAGTPTWETESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFGA 360  
 Db 301 GEWSEWSPKAGTPTWETESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFGA 360

Qy 361 GLVLGGQFMVPPGEGDS-----KD-----VAAPHRQPLT----- 389  
 Db 361 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 420

Qy 390 -----SSERIDKQIRYILDGIALRKETCNKSNWCE 420  
 Db 421 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNNTKVDKKV-----EPKSCDKTHTCP 470

Qy 421 --SSKEALAENLNLPKMAEKDGFSGFNEETCLVKIIT--GLLFEFVVVLELQ--N 472  
 Db 471 PCFAPELLGGPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 530

Qy 473 RFESSEEQARAVQMSTKVL 491  
 Db 531 KTKPREEQYNSTYRVVSVL 549

RESULT 8  
 AAW70797  
 ID AAW70797 standard; protein; 592 AA.  
 XX  
 AC AAW70797;  
 XX  
 DT 03-FEB-1999 (first entry)  
 XX Human interleukin-6R-alpha-Fc.  
 XX  
 DE gp130; cytokine antagonist; interleukin; gamma-interferon;  
 KW granulocyte macrophage colony-stimulating factor; J peptide;  
 KW transforming growth factor-beta.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Protein 1..358  
 FT /note= "human IL-R-alpha"  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Misc-difference 2  
 FT /label= L2V  
 FT /note= "changed to accommodate a Kozak sequence"  
 FT Misc-difference 359..360  
 FT /note= "Ala-Gly bridge"  
 FT Protein 361..592  
 FT /note= "Fc domain of human IgG1"  
 FT Disulfide-bond 371..374  
 XX US5844099-A.  
 XX  
 PD 01-DEC-1998.  
 XX  
 PF 27-NOV-1995; 95US-00563105.  
 XX  
 PR 20-OCT-1993; 93US-00140222.  
 XX  
 PA (REG- ) REGENERON PHARM INC.  
 XX  
 PI Yancopoulos GD, Stahl N, Economides A;  
 XX WPI; 1999-044669/04.  
 DR  
 XX Cytokine antagonists - comprising extracellular domains of specificity-  
 PT determining and signal-transducing components of cytokine receptor.  
 XX

Example 3; Fig 5; 46pp; English.

The present sequence represents the amino acid sequence of human interleukin (IL)-6R-alpha-Fc. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte macrophage colony-stimulating factor (GM-CSF), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines

Sequence 592 AA;

Query Match 66.2%; Score 1927.5; DB 2; Length 592;  
 Best Local Similarity 72.8%; Pred. No. 4.9e-124;  
 Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;  
 QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
 DB 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGPAGTVHLLVDVPEEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGPAGTVHLLVDVPEEPQLS 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPDPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPDPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWGLRHVVQLRAQERFGQ 300  
 DB 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDWGLRHVVQLRAQERFGQ 300  
 QY 301 GEWSEWSPFAMGTPWTESSRPPAEVNEVTPMQALTTNKDDNILLFRDSANATSLPVERG- 359  
 DB 301 GEWSEWSPFAMGTPWTESSRPPAEVNEVTPMQALTTNKDDNILLFRDSANATSLPVDAG 360  
 QY 360 -----AGLVLGQ-----PMVPPGSDSKDAAPHRQPL-----TSSE 393  
 DB 361 BPKSCDKTHTCPPCPAPELLGGPSVFLPPPKP-----KDTLMISRTPEVTCVVDVSHED 415  
 QY 394 IDKQIRYILDGI-----SALRKETCNKSNWCESSKEALAEENLN-----LPK 435  
 DB 416 PEVFPNFWVGVGVHNAKTPREBOYNSTYRVVSVLTVLHQLWGLKGYKCKVSNKALPA 475  
 QY 436 MAEKDGCQFSQFNBER-----TCLVKTIITGLLEPEVYLEYLQN 472  
 DB 476 PIEKTIKAKGQPREQVYVTLPPSDELTKQVSLTCLVK---GFYPSDIAVEWESN 529

RESULT 9

AA92185  
 ID AA92185 standard; protein; 592 AA.

AC AA92185;

DT 01-AUG-2000 (first entry)

DE Human IL-6R-alpha-Fc fusion protein.

KW IL-6R-alpha-Fc; cytokine; antagonist; CNTF; receptor; fusion protein;  
 cytotatic; immunomodulator; osteopathic.

OS Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Protein 1..358  
 FT Peptide /label= IL-6R-alpha  
 FT Peptide 1..19  
 FT Peptide /label= signal\_peptide  
 FT Peptide 359..360  
 FT Protein /note= "Ala-Gly bridge"  
 FT Protein 361..592  
 FT Disulfide-bond /label= IgG1\_Fc\_domain  
 FT Disulfide-bond 371  
 FT Disulfide-bond /note= "forms inter-chain disulfide bridge that link two  
 FT Disulfide-bond 374 Fc domains"  
 FT Disulfide-bond /note= "forms inter-chain disulfide bridge that link two  
 FT Disulfide-bond 374 Fc domains"  
 XX WO200018932-A2.  
 XX 06-APR-2000.  
 XX 22-SEP-1999; 99WO-US022045.  
 XX 25-SEP-1998; 98US-0101858P.  
 PR 19-MAY-1999; 99US-00313942.  
 XX (REGE-) REGENERON PHARM INC.  
 XX Stahl N, Yancopoulos GD;  
 FI WPI; 2000-293165/25.  
 XX Isolated nucleic acid molecule for treating cytokine-related diseases or  
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to  
 FT form a nonfunctional complex.  
 XX Example 3; Fig 5; 152pp; English.  
 The invention concerns production of antagonists to any cytokine that  
 CC utilizes an alpha specificity determining component, which when combined  
 CC with the cytokine, binds to a first beta signal transducing component to  
 CC form a non-functional intermediate which then binds to a second beta  
 CC signal transducing component causing beta-receptor dimerization, the  
 CC soluble alpha specificity determining component of the receptor (SR-  
 CC alpha) and the extracellular domain of the first beta signal transducing  
 CC component of the cytokine receptor (beta-1) are combined to form  
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by  
 CC binding the cytokine to form a non-functional complex. The receptor  
 CC components are shared by cytokines such as the CNTF (Ciliary neurotrophic  
 CC factor) family of cytokines. The invention provides the basis for the  
 CC development of IL-6 antagonists, as they show that if, in the presence of  
 CC a ligand, a non-functional intermediate complex, consisting of the  
 CC ligand, its alpha receptor and its beta-1 receptor component, can be  
 CC formed, it will effectively block the action of the ligand. Effective  
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular  
 CC domains of the alpha specificity determining components of their  
 CC receptors and the extracellular domain of gp130. The resultant  
 CC heterodimers, function as high-affinity traps, rendering the cytokine  
 CC inaccessible to form a signal transducing complex with the native  
 CC membrane-bound forms of their receptor. The nucleic acids and  
 CC polypeptides are useful for treating cytokine-related diseases or  
 CC disorders such as osteoporosis and primary and secondary effects of  
 CC cancer including multiple myeloma or cachexia  
 XX SQ Sequence 592 AA;

Query Match 66.2%; Score 1927.5; DB 3; Length 592;  
 Best Local Similarity 72.8%; Pred. No. 4.9e-124;  
 Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;  
 QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
 DB 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60

```

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
QY 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTQFGCGILQPPPPANITVTAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTQFGCGILQPPPPANITVTAVARNPRLSVTWQD 240
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVQLRAQEFQ 300
QY 301 GESEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDFG- 359
DB 301 GESEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG 360
QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHROPL-----TSSE 393
DB 361 EPKSCDKTHTCCPCPAPPELLGGPSVFLFPKP-----KDTLMSRTPEVTCVVVDVSHED 415
QY 394 IDKQIRYLDGI-----SALRKETCNKSNMCSSKEALAENNLN-----LPK 435
DB 394 IDKQIRYLDGI-----SALRKETCNKSNMCSSKEALAENNLN-----LPK 435
QY 416 PEVKFNWYDGVGVHNAKTKEPEQYNSYTRVSVLTLVHQLDGLNGKEYCKVSNKALPA 475
DB 416 PEVKFNWYDGVGVHNAKTKEPEQYNSYTRVSVLTLVHQLDGLNGKEYCKVSNKALPA 475
QY 436 MAEKDGCFCQSGFNEE-----TCLVKILITGLLEFEVYLEYLN 472
DB 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

RESULT 10
ABW02165
ID ABW02165 standard; protein; 592 AA.
AC AC
XX ABW02165;
XX
DT 12-FEB-2004 (first entry)
DE Human IL-6Ralpha-Fc protein.
KW Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
KW cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT /note= "Human mature IL-6Ralpha-Fc protein"
FT Region 359..360
FT /note= "Ala-Gly bridge"
FT Domain 361..592
FT /note= "Human IgG1 Fc domain"
FT Disulfide-bond 371..374
FT /note= "Inter-chain disulphide bridge"
XX
XX US2003143697-A1.
XX
XX 31-JUL-2003.
XX
XX 28-OCT-2002; 2002US-00282162.
XX
XX 22-SEP-1999; 99WO-US022045.
XX 22-MAR-2001; 2001US-00787835.
XX
XX (STAHL/) STAHL N.
XX (YANC/) YANCOPOULOS G D.

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PI Stahl N, Yancopoulos GD;
XX
XX WPI; 2003-851784/79.
XX
XX New nucleic acid molecules encoding fusion polypeptides capable of
XX binding a cytokine to form a non-functional complex, useful for treating
XX cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
XX or osteoporosis.
XX
XX Example 3; Fig 5; 300pp; English.
XX
XX The present invention provides a novel fusion polypeptide capable of
XX binding a cytokine to form a nonfunctional complex. The invention is
XX useful for identifying agonists or antagonists of cytokine receptors and
XX for treating cytokine-related diseases or disorders e.g. cancer,
XX cachexia, arthritis and osteoporosis. The present sequence is human IL-
XX 6Ralpha-Fc protein
XX
XX Sequence 592 AA;
XX
Query Match 66.2%; Score 1927.5; DB 7; Length 592;
Best Local Similarity 72.8%; Pred. No. 4.9e-124;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;
QY 1 MLAVGCALLAALAAFGAALAPRRCPAQEVARGLVTSLPDGSVTLTCGVPEDNATVHW 60
DB 1 MVAVGCALLAALAAFGAALAPRRCPAQEVARGLVTSLPDGSVTLTCGVPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
QY 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTQFGCGILQPPPPANITVTAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTQFGCGILQPPPPANITVTAVARNPRLSVTWQD 240
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHHCVIHDWSGLRHVVQLRAQEFQ 300
QY 301 GESEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDFG- 359
DB 301 GESEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG 360
QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHROPL-----TSSE 393
DB 361 EPKSCDKTHTCCPCPAPPELLGGPSVFLFPKP-----KDTLMSRTPEVTCVVVDVSHED 415
QY 394 IDKQIRYLDGI-----SALRKETCNKSNMCSSKEALAENNLN-----LPK 435
DB 394 IDKQIRYLDGI-----SALRKETCNKSNMCSSKEALAENNLN-----LPK 435
QY 416 PEVKFNWYDGVGVHNAKTKEPEQYNSYTRVSVLTLVHQLDGLNGKEYCKVSNKALPA 475
DB 416 PEVKFNWYDGVGVHNAKTKEPEQYNSYTRVSVLTLVHQLDGLNGKEYCKVSNKALPA 475
QY 436 MAEKDGCFCQSGFNEE-----TCLVKILITGLLEFEVYLEYLN 472
DB 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

RESULT 11
AA92196
ID AA92196 standard; protein; 468 AA.
XX
XX AA92196;
XX
XX 01-AUG-2000 (first entry)
XX
XX Human IL-6R-alpha-kappa fusion protein.
XX
XX IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
XX fusion protein; cytostatic; immunomodulator; osteopathic.
XX

```



XX Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..358 /label= IL-6R-alpha  
FT Peptide 359..360 /note= "Ala-Gly bridge"  
FT Protein 361..468 /label= kappa\_domain  
XX  
XX WO200018932-A2.  
FN  
XX  
XX 06-APR-2000.  
XX  
XX 22-SEP-1999; 99WO-US022045.  
XX  
XX 25-SEP-1998; 98US-0101858P.  
PR 19-MAY-1999; 99US-00313942.  
XX  
XX (REGE-) REGENERON PHARM INC.  
PA  
XX  
XX Stahl N, Yancopoulos GD;  
PI  
XX  
XX WPI; 2000-293165/25.  
DR  
XX  
XX Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.  
XX  
XX Example 4; Page; 152pp; English.  
XX  
XX The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia  
XX  
XX Sequence 468 AA;  
Query Match 66.1%; Score 1923.5; DB 3; Length 468;  
Best Local Similarity 95.5%; Pred. No. 6.8e-124;  
Matches 360; Conservative 5; Mismatches 11; Indels 1; Gaps 1;  
QY 1 MVAUGCALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
DB 1 MVAUGCALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
QY 61 VLKRPAGSHPSRWAGMGRLLRLLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS 120  
DB 61 VLKRPAGSHPSRWAGMGRLLRLLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180  
QY 181 PEGDSSEYIYVMCVASSVSGSKFTOTFOCGIILQPPPPANITVTAVARNRWLSVTWQD 240  
DB 181 PEGDSSEYIYVMCVASSVSGSKFTOTFOCGIILQPPPPANITVTAVARNRWLSVTWQD 240  
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFGQ 300  
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFGQ 300  
QY 301 GENSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVBFG 359  
DB 301 GENSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVBQDAG 360  
QY 360 AGLVLGGQPMVPVPGED 376  
DB 361 SGTVAAPSVFIFPPSDE 377  
RESULT 12  
AAI92197  
ID AAY92197 standard; protein; 477 AA.  
XX  
XX AAY92197;  
XX  
XX 01-AUG-2000 (first entry)  
DT Human IL-6R-alpha-j-kappa fusion protein.  
XX  
XX IL-6R-alpha-j-kappa; cytokine; antagonist; CNTF; receptor;  
XX fusion protein; Cytostatic; Immunomodulator; osteopathic.  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX WO200018932-A2.  
XX  
XX 06-APR-2000.  
XX  
XX 22-SEP-1999; 99WO-US022045.  
XX  
XX 25-SEP-1998; 98US-0101858P.  
PR 19-MAY-1999; 99US-00313942.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Stahl N, Yancopoulos GD;  
XX  
XX WPI; 2000-293165/25.  
XX  
XX Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.  
XX  
XX Example 4; Page; 152pp; English.  
XX  
XX The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia  
XX  
XX Sequence 468 AA;  
Query Match 66.1%; Score 1923.5; DB 3; Length 468;  
Best Local Similarity 95.5%; Pred. No. 6.8e-124;  
Matches 360; Conservative 5; Mismatches 11; Indels 1; Gaps 1;  
QY 1 MVAUGCALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
DB 1 MVAUGCALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60  
QY 61 VLKRPAGSHPSRWAGMGRLLRLLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS 120  
DB 61 VLKRPAGSHPSRWAGMGRLLRLLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS 120

formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia

Sequence 477 AA;

Query Match	66.0%;	Score 1922;	DB 3;	Length 477;
Best Local Similarity	81.9%;	Pred. No. 8.9e-124;		
Matches 376;	Conservative 13;	Mismatches 28;	Indels 42;	Gaps 6;
Qy	1	MLAVGCALLAALAAAPGAALAPRCRPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW	60	
Db	1	MVAVGCALLAALAAAPGAALAPRCRPAQAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW	60	
Qy	61	VLKPAAGSHPSRWAGHGRLLLSVOLHDSGNVSCYRAGPAGTAVHLLVDVPPPEEQLS	120	
Db	61	VLKPAAGSHPSRWAGHGRLLLSVOLHDSGNVSCYRAGPAGTAVHLLVDVPPPEEQLS	120	
Qy	121	CFRKSPLSNVVCEWGPBSTSLTTKAVLLVRKFQNSPAEDQFQPCQYSQESQKFSQCLAV	180	
Db	121	CFRKSPLSNVVCEWGPBSTSLTTKAVLLVRKFQNSPAEDQFQPCQYSQESQKFSQCLAV	180	
Qy	181	PEGDSSEYIYVSMCVASSVGSKFSTQTFQGGCIIQDPDPANITTVARNPRWLSVTWQD	240	
Db	181	PEGDSSEYIYVSMCVASSVGSKFSTQTFQGGCIIQDPDPANITTVARNPRWLSVTWQD	240	
Qy	241	PHSNWSSFYRLRPELRYRAERSKFTFTTMVKDLOHHCVIHDWNSGLRHVQLRAQEEFGQ	300	
Db	241	PHSNWSSFYRLRPELRYRAERSKFTFTTMVKDLOHHCVIHDWNSGLRHVQLRAQEEFGQ	300	
Qy	301	GEWSEWSEPAAGTPTWTSRSPPAEENVESTPMQALTTNKDDNIIIFRDSANATSLPVE---	357	
Db	301	GEWSEWSEPAAGTPTWTSRSPPAEENVESTPMQALTTNKDDNIIIFRDSANATSLPVDQAG	360	
Qy	358	-FGAGLVILGGQFMVPVPGEDSKDVAAPHROPLTTSERIDKOIRYILDGISALRKETCNKS	416	
Db	361	TFGGCTKV-----EIKTVAAASVFIFPPS---DEQK-----SGTASVVCLLN	400	
Qy	417	NMCESSEKALAEANNLNIAPKWA-----EKDQCFCQSGFNEET	451	
Db	401	NF-----YPRAKVQWVKDNLALQSGNSQES	425	

RESULT 13  
AAP90284  
ID AAP90284 standard; protein: 468 AA.

AC	RAP90284;
XX	
XX	
DT	25-MAR-2003 (revised)
DT	31-MAR-1992 (first entry)
XX	
XX	
DE	Sequence of a receptor protein for human B cell stimulating factor-2
DE	(BSF2 receptor).

XX  
KW  
B cell; immune disorder; therapy; diagnosis; prophylaxis.

OS Homo sapiens.

XX	Key	Location/Qualifiers
AA	Region	2. .22
FF		/label= hydrophobic region
FT	Region	362. .386
FT		/label= hydrophobic region
FT		

PN EP325474-A.

[illegible]

KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;  
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;  
 KW disease; intracellular.  
 XX Synthetic.  
 OS  
 XX JP05091892-A.  
 PN  
 XX 16-APR-1993.  
 PD  
 XX  
 PF 02-OCT-1991; 91JP-00255521.  
 XX  
 XX 02-OCT-1991; 91JP-00255521.  
 PR  
 XX (KISH/) KISHIMOTO C.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 PA (TOYU ) TOSOH CORP.  
 XX  
 XX WPI; 1993-161739/20.  
 DR N-PSDB; AAQ41746.  
 DR  
 XX New interleukin-6 receptor deriv. - for treating diseases caused by IL-6,  
 PT e.g. multiple myeloma.  
 XX  
 XX Disclosure; Page 10-12; 23pp; Japanese.  
 PS  
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants of  
 CC the receptor lacking either the immunoglobulin-like domain or the  
 CC transmembrane and intracellular domain have IL-6 binding ability and  
 CC signal transfer ability. Either the full length or truncated IL-6  
 CC receptors may be used for diseases caused by IL-6 such as multiple  
 CC myeloma  
 XX  
 XX Sequence 468 AA;

Query Match 65.8%; Score 1917; DB 2; Length 468;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-123;  
 Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;  
 QY 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHW 60  
 DB 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120  
 QY 121 CFRKPSLNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEQDFQPCQYSESQKFSQCLAV 180  
 DB 121 CFRKPSLNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEQDFQPCQYSESQKFSQCLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEEFGQ 300  
 DB 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEEFGQ 300  
 QY 301 GEWSWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360  
 DB 301 GEWSWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360  
 QY 361 G-----LVLG 366  
 DB 361 SVPLPTFLVAGG 372

RESULT 15  
 AAB36655  
 ID AAB36655 standard; protein; 468 AA.  
 XX  
 AC AAB36655;

XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human IL-6 receptor subunit alpha protein SEQ ID NO:12.  
 XX  
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;  
 KW modulating cell proliferation; diagnosis; detection; drug screening;  
 KW immunological disorder.  
 XX  
 OS Homo sapiens.  
 XX WO200073451-A1.  
 PN  
 XX 07-DEC-2000.  
 PD  
 XX 30-MAY-2000; 2000WO-US014867.  
 PF  
 XX 01-JUN-1999; 99US-00322913.  
 PR  
 XX (SCHE ) SCHERING CORP.  
 PA  
 XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;  
 PI WPI; 2001-061536/07.  
 XX  
 XX Novel composition comprising DNAX cytokine receptor subunit polypeptide  
 PT useful for regulating immune system function and for treating  
 PT immunological disorders.  
 XX  
 PS Disclosure; Page 13-15; 93pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a  
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The  
 CC DCRS2 polypeptide is useful for binding ligands and for preparing  
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell  
 CC proliferation, for diagnostic and therapeutic applications, for detecting  
 CC presence of their ligands and in drug screening assays. It is also useful  
 CC for treating conditions such as immunological disorders. The present  
 CC sequence represents a cytokine receptor subunit protein which is given in  
 CC an alignment of various cytokine receptor subunits in the exemplification  
 CC of the present invention  
 XX  
 XX Sequence 468 AA;

Query Match 65.8%; Score 1917; DB 4; Length 468;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-123;  
 Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;  
 QY 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHW 60  
 DB 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120  
 DB 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTAVHLLVDVPPPEPQLS 120  
 QY 121 CFRKPSLNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEQDFQPCQYSESQKFSQCLAV 180  
 DB 121 CFRKPSLNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEQDFQPCQYSESQKFSQCLAV 180  
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD 240  
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTAVARNRWLSVTWQD 240  
 QY 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEEFGQ 300  
 DB 241 PHSWNSFFYRLRFELRYRAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEEFGQ 300  
 QY 301 GEWSWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360  
 DB 301 GEWSWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360  
 QY 361 G-----LVLG 366

Db 361 SVPLPTFLVAGG 372  
|||

Search completed: September 7, 2006, 22:57:55  
Job time : 196 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 22:58:10 ; Search time 42 Seconds  
(without alignments)  
1266.854 Million cell updates/sec

Title: US-09-462-416A-13  
Perfect score: 2912  
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSFKFLOSSLRALRQM 553

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1917	65.8	468	1 A41242	interleukin-6 rece
2	954	32.8	440	2 JLO144	interleukin-6 rece
3	953.5	32.7	460	2 JLO145	interleukin-6 rece
4	947.5	32.5	212	1 IVHUB2	interleukin-6 prec
5	856.5	29.4	462	1 A37986	interleukin-6 rece
6	580.5	19.9	208	2 T09216	interleukin-6 prec
7	569	19.5	212	2 I46621	prointerleukin 6 -
8	568	19.5	212	2 I46590	interleukin 6 - pi
9	480.5	16.5	208	1 A56610	interleukin-6 prec
10	478.5	16.4	207	1 I46084	interleukin 6 - ca
11	474.5	16.3	208	1 S29549	interleukin-6 - sh
12	397	13.6	211	2 A34247	interleukin-6 prec
13	376	12.9	211	1 ICM56	interleukin-6 prec
14	339.5	11.7	422	2 I37891	interleukin-11 rec
15	335	11.5	432	2 I48343	interleukin-11 rec
16	314.5	10.8	372	2 I58141	ciliary neurotroph
17	309.5	10.6	372	1 URHUCN	ciliary neurotroph
18	302.5	10.4	362	2 S60614	growth promoting a
19	226	7.8	53	2 IS3394	soluble interleuki
20	198.5	6.8	328	2 A38957	interleukin 12B pr
21	180	6.2	831	2 JQ1655	prolactin receptor
22	171.5	5.9	830	2 I50455	prolactin receptor
23	171	5.9	581	2 I45971	prolactin receptor
24	170	5.8	918	2 A4257	interleukin-6 sign
25	167.5	5.8	917	2 I43699	glycoprotein 130 -
26	164.5	5.6	918	2 A36337	membrane glycoprot
27	160	5.5	616	2 A30304	prolactin receptor
28	159	5.5	310	2 A29884	prolactin receptor
29	159	5.5	412	2 A41070	prolactin receptor

## ALIGNMENTS

### RESULT 1

A41242

interleukin-6 receptor precursor - human

N:Contains: interleukin-6 receptor, soluble form

C:Species: Homo sapiens (man)

C>Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text\_change 09-Jul-2004

C:Accession: A41242; J00080; S17468; A61459; S14621

R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988

A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.

A:Reference number: A41242; MUID:88305347; PMID:3136546

A:Accession: A41242

A:Molecule type: mRNA

A:Residues: 1-468 <YAM>

A:Cross-references: UNIPROT:P08887; UNIPARC:UPI00000358BA; GB:M20566; NID:G33845; PIDN:R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988

A:Title: Molecular structure of interleukin 6 receptor.

A:Reference number: J00080

A:Accession: J00080

A:Molecule type: mRNA

A:Residues: 1-468 <YA2>

A:Cross-references: UNIPARC:UPI00000358BA

R:Schootink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, Biochem. J. 277, 659-664, 1991

A:Title: Structural and functional studies on the human hepatic interleukin-6 receptor

A:Reference number: S17468; MUID:91336983; PMID:1872801

A:Accession: S17468

A:Molecule type: mRNA

A:Residues: 1-468 <SCH>

A:Cross-references: UNIPARC:UPI00000358BA; EMBL:X58298; NID:G32580; PIDN:CAA41231.1; P:R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989

A:Title: Soluble cytokine receptors are present in normal human urine.

A:Reference number: A61459; MUID:90010793; PMID:2529343

A:Accession: A61459

A:Molecule type: protein

A:Residues: 20-49 <NOV>

A:Cross-references: UNIPARC:UPI000002CF0B

C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, and C:Genetics: This growth factor receptor does not have a tyrosine kinase domain.

A:Gene: GDB:IL6R

A:Cross-references: GDB:127966; OMIM:147880

A:Map position: 1q21-1q21

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immun

C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-468/Product: interleukin-6 receptor #status predicted <MAT>

F:20-363/Domain: extracellular #status predicted <EXT>

F:40-98/Domain: immunoglobulin homology <IMM2>

lactogen receptor  
prolactin receptor  
interleukin 12 p40  
prolactin receptor  
prolactin receptor  
prolactin receptor  
prolactin receptor  
prolactin receptor  
protein-tyrosine k  
Down syndrome cell  
receptor tyrosine  
prolactin receptor  
prolactin receptor  
prolactin receptor  
leptin receptor, i  
protein-tyrosine k  
granulocyte colony

30 159 5.5 610 2 A34631  
31 159 5.5 610 2 A36116  
32 158.5 5.4 335 2 I72789  
33 155 5.3 292 2 I77525  
34 155 5.3 303 2 I77524  
35 155 5.3 608 2 I53269  
36 155 5.3 630 2 I51086  
37 149 5.1 890 1 A53743  
38 144 4.9 1896 2 T08851  
39 140.5 4.8 882 2 I38912  
40 138 4.7 288 2 B59405  
41 138 4.7 376 2 A59405  
42 138 4.7 622 2 A40144  
43 133.5 4.6 895 2 S74225  
44 132.5 4.6 880 1 J4166  
45 131 4.5 837 2 A34898

F;121-309/Domain: cytokine receptor homology <CRS>  
E;364-386/Domain: transmembrane #status predicted <TM>  
F;387-468/Domain: intracellular #status predicted <INT>  
F;47-96/Disulfide bonds: #status predicted  
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.8%; Score 1917; DB 1; Length 468;  
Best Local Similarity 96.8%; Pred. No. 1.4e-128;  
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNSCYRAGRAGTGHLLVDVPPPEPQLS 120  
Db 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNSCYRAGRAGTGHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGGILQPDPPANITVTAVARNPRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRPELRYRAERSKFTFTMWVKDLOHCHVHDWGLRHVVQLRAQEFQ 300  
Db 241 PHSWNSFYRLRPELRYRAERSKFTFTMWVKDLOHCHVHDWGLRHVVQLRAQEFQ 300

Qy 301 GEWSEWSPAMGTPTWTSERSPPAENEVSTPMQALTNKDDNILLFRSDANATSLPVFEGA 360  
Db 301 GEWSEWSPAMGTPTWTSERSPPAENEVSTPMQALTNKDDNILLFRSDANATSLPVQDSS 360

Qy 361 G-----LVLG 366  
Db 361 SVPLPTFLVAGG 372

RESULT 2  
JL0144  
interleukin-6 receptor precursor (clone lambda P1) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: JL0144  
R;Sugita, T.; Totoku, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.  
J. Exp. Med. 171, 2001-2009, 1990  
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene  
A;Reference number: JL0144; MUID:90278354; PMID:2112585  
A;Accession: JL0144  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-440 <SUG>  
A;Cross-references: UNIPROT:P22272; UNIPARC:UPI000011F2D9; GB:X51976; NID:G53548; PIDN:C  
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-44/Product: interleukin-6 receptor #status predicted <MAT>  
F;40-94/Domain: immunoglobulin homology <IMM>  
F;117-306/Domain: cytokine receptor homology <CRS>  
F;358-385/Domain: transmembrane #status predicted <TRA>

Query Match 32.8%; Score 954; DB 2; Length 440;  
Best Local Similarity 48.0%; Pred. No. 3.6e-60;  
Matches 195; Conservative 50; Mismatches 127; Indels 34; Gaps 7;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MLTVGCTLLVALLAALPAVALVGLSCRALEVANGTIVSLPGATVTLICPGKEAGNVTIHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNSCYRAGRAGTGHLLVDVPPPEPQLS 120  
Db 61 VY-----SGSQNRWTTTGTNLVLRDVLSDTGDYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLA 179  
Db 117 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLA 176

Qy 180 VPEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGGILQPDPPANITVTAVARNPRWLSVTWQ 239  
Db 177 ILEGDKYHIVSLCVANSVSGSKSHNEAFHSLKMWQDPPANLVVSAIPGRPRWLKYSWQ 236

Qy 240 PHSWNSFYRLRPELRYRAERSKFTFTMWVKDLOHCHVHDWGLRHVVQLRAQEFQ 299  
Db 237 HPETWDPYLLQPOLRYRPMWSKEFTVLLLPVAAQYCVIHDALRGVKKVQVQVQKEELD 296

Qy 300 QGEWSEWSPAMGTPTWTSERSPPAENEVSTPMQALTNKDDNILLFRSDANATSL--PV 356  
Db 297 LGQWSEWSPVETGPTWIAEPRTTPA-GILWNPTQVSVEDSANHEDQYESSTEATSVLAPV 355

Qy 357 EFAGAG-----LVLGQGF-----MPVPPGSDS 377  
Db 356 QESSMSLPTFLVAGGSLAFGLLCLVFIILCWEPHPSPLQDGADS 401

RESULT 3  
JL0145  
interleukin-6 receptor precursor (clone lambda 301) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: JL0145; S14543  
R;Sugita, T.; Totoku, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.  
J. Exp. Med. 171, 2001-2009, 1990  
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene  
A;Reference number: JL0144; MUID:90278354; PMID:2112585  
A;Accession: JL0145  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-460 <SUG>  
A;Cross-references: UNIPROT:P22272; UNIPARC:UPI0000022D4B; GB:X51975; NID:G49725; PIDN:  
A;Experimental source: clone lambda 301  
A;Submitted to: EMBL Data Library, July 1990  
A;Description: Cloning and expression of murine IL-6 receptor.  
A;Reference number: S14543  
A;Accession: S14543  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-373,'R',375-460 <FIO>  
A;Cross-references: UNIPARC:UPI000016CE46; EMBL:X53802; NID:G52692; PIDN:CAA37810.1; PI  
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immun  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-46/Product: interleukin-6 receptor #status predicted <MAT>  
F;40-94/Domain: immunoglobulin homology <IMM>  
F;117-306/Domain: cytokine receptor homology <CRS>  
F;358-385/Domain: transmembrane #status predicted <TRA>

Query Match 32.7%; Score 953.5; DB 2; Length 460;  
Best Local Similarity 50.8%; Pred. No. 4.2e-60;  
Matches 191; Conservative 49; Mismatches 121; Indels 15; Gaps 6;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
Db 1 MLTVGCTLLVALLAALPAVALVGLSCRALEVANGTIVSLPGATVTLICPGKEAGNVTIHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRSVLQHDGNSCYRAGRAGTGHLLVDVPPPEPQLS 120  
Db 61 VY-----SGSQNRWTTTGTNLVLRDVLSDTGDYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLA 179  
Db 117 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAE-DFQEPQCOYSQESQKFSQCOLA 176

Qy 180 VPEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGGILQPDPPANITVTAVARNPRWLSVTWQ 239  
Db 177 ILEGDKYHIVSLCVANSVSGSKSHNEAFHSLKMWQDPPANLVVSAIPGRPRWLKYSWQ 236

Db 177 ILEGGKVHYIVSLCVANSVSGSKSHNEAFHSLKMWQDPPLANVLVSAIFCRPRWLKVSQ 236

QY 240 DPHSNWSSFYRLRFLRYRAERSKTTTWMXDLQHCHCVIHDAMSLRHVVOLRAQEFG 299

Db 237 HETWDPYSYLLQFQRLRYRPSWKEFTVLLPVAQCIVHDLRGVKKVQVRGKEILD 296

QY 300 QGEWSWSPSPMGTPM-TESRSPPAENVESTPMQALTTNKDDNNILFRDSANATSL--PV 356

Db 297 LGQWSWSPSEVGTGPIAEPRTTPA-GILWNPQTQSVSDSANHDDQYESSTTSATSLVAPV 355

QY 357 EFGAG-----LVGG 366

Db 356 QESSMSLPTFLVAGG 371

RESULT 4

IVHUB2

interleukin-6 precursor [validated] - human

N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell on factor

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27

R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimoto

EMBO J. 6, 2939-2945, 1987

A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene

A;Reference number: A32648; MUID:88082664; PMID:3500852

A;Accession: A32648

A;Molecule type: DNA

A;Residues: 1-212 <YAS>

A;Cross-references: UNIPROT:P05231; UNIPARC:UPI000002C4A6; GB:X04430; NID:G29494; PIDN:C

A;Note: the authors translated the codon CAG for residue 130 as Glu

R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.

EMBO J. 5, 2529-2537, 1986

A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a disti

A;Reference number: A91051; MUID:87053818; PMID:3023045

A;Accession: A25692

A;Molecule type: mRNA

A;Residues: 1-212 <ZIL>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G

R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura

i, T.; Kishimoto, T.

Nature 324, 73-76, 1986

A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocy

A;Reference number: A93387; MUID:87065033; PMID:3491322

A;Accession: A26966

A;Molecule type: mRNA

A;Residues: 1-212 <HIR>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04602; NID:G33849; PIDN:CAA28268.1; PID:G

R;Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.

Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989

A;Title: Deletion of 3' untranslated region of human BSP-2 mRNA causes stabilization of

A;Reference number: A33515; MUID:89391958; PMID:2789513

A;Accession: A33515

A;Molecule type: mRNA

A;Residues: 1-212 <TON>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M29150; NID:gi186349; PIDN:AAA59154.1; PID:

R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.

Eur. J. Biochem. 159, 625-632, 1986

A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h

A;Reference number: A25801; MUID:87004603; PMID:3758081

A;Accession: A25801

A;Molecule type: DNA; mRNA

A;Residues: 1-212 <HAE>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04403

A;Experimental source: fibroblast

R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986

A;Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA

A;Reference number: A25921; MUID:87067433; PMID:3538015

A;Accession: A25921

A;Molecule type: mRNA

A;Residues: 1-212 <MAY>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M14584; NID:gi184628; PIDN:AAA52728.1; PI

R;Wong, G.G.; Mitek-Glannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.

Behring Inst. Mitt. 83, 40-47, 1988

A;Title: Interleukin 6; Identification as a hematopoietic colony-stimulating factor.

A;Reference number: I52193; MUID:89193317; PMID:3266463

A;Accession: I52193

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-212 <WON>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M54894; NID:gi186351; PIDN:AAC41704.1; PI

R;Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.

J. Immunol. 139, 4116-4121, 1987

A;Title: Molecular cloning and expression of hybridoma growth factor in Escherichia co

A;Reference number: I56003; MUID:88088768; PMID:3320204

A;Accession: I56003

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-212 <BRA>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M18403; NID:gi184631; PIDN:AAAS2729.1; PI

R;Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.

J. Immunol. 140, 1534-1541, 1988

A;Title: Separation and comparison of two monokines with lymphocyte-activating factor

A;Reference number: A92816; MUID:88154445; PMID:3279116

A;Accession: A27601

A;Molecule type: protein

A;Residues: 28-51,'X','53-57,'X','59,'X','61 <VAN1>

A;Cross-references: UNIPARC:UPI0000173666

A;Accession: B27601

A;Molecule type: protein

A;Residues: 30-56,'XX','59-61,'X','63 <VA2>

A;Cross-references: UNIPARC:UPI0000173666

R;Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.

J. Immunol. 144, 1808-1816, 1990

A;Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involve

A;Reference number: A60400; MUID:90171574; PMID:2307841

A;Accession: A60400

A;Molecule type: protein

A;Residues: 30-43 <YAM>

A;Cross-references: UNIPARC:UPI0000173668

R;Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu

Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987

A;Title: Human beta-cell differentiation factor defined by an anti-peptide antibody an

A;Reference number: A29085; MUID:87092370; PMID:3491991

A;Accession: A29085

A;Molecule type: protein

A;Residues: 29-42 <HIR2>

A;Cross-references: UNIPARC:UPI0000173669

R;Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.;

Anticancer Res. 11, 961-968, 1991

A;Title: Purification and characterization of human fibroblast derived differentiation

A;Reference number: A61159; MUID:91290785; PMID:1648338

A;Accession: A61159

A;Molecule type: protein

A;Residues: 30-42 <NOD>

A;Cross-references: UNIPARC:UPI000017366A

A;Experimental source: fibroblast

R;Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.

J. Mol. Cell. Immunol. 4, 203-212, 1989

A;Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor

A;Reference number: A61462; MUID:90121567; PMID:2610854

A;Accession: A61462

A;Molecule type: protein

A;Residues: 28-48 <MIN>

A;Cross-references: UNIPARC:UPI000017366B

A;Experimental source: leukocyte-conditioned medium

R;May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.

Cytokine 3, 204-211, 1991

A;Title: Marked cell-type-specific differences in glycosylation of human interleukin-6

A;Reference number: A48419; MUID:91355644; PMID:1883960

A;Accession: A48419

A;Molecule type: protein

A;Residues: 30-37,'X','39-40 <MAY2>

A;Cross-references: UNIPARC:UPI000017366C

















DR PROSITE; PS50835; IG LIKE; 1.  
 KW 3D-structure; Alternative splicing; Direct protein sequencing;  
 Query Match 65.8%; Score 1917; DB 1; Length 468;  
 Best Local Similarity 96.8%; Pred. No. 9.8e-131; Indels 6; Gaps 1;  
 Matches 360; Conservative 2; Mismatches 4;  
 QY 1 MLAVGCALLAALAAAPGALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 DB 1 MLAVGCALLAALAAAPGALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRPAQVTHLLVDVPPPEPOL 120  
 DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRPAQVTHLLVDVPPPEPOL 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESKQSCQLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESKQSCQLAV 180  
 QY 181 PEGDSSFFIVSMCVASSVSGSKFSTQTQGGCGILQDPPANITVTAVARNPRLSVTWQD 240  
 DB 181 PEGDSSFFIVSMCVASSVSGSKFSTQTQGGCGILQDPPANITVTAVARNPRLSVTWQD 240  
 QY 241 PHSWNSFYRLRFELRYRAERSKFTTWWVXDLOHHCYVHDWAGSLRHVVQLRAQEERFG 300  
 DB 241 PHSWNSFYRLRFELRYRAERSKFTTWWVXDLOHHCYVHDWAGSLRHVVQLRAQEERFG 300  
 QY 301 GEWSSEPMAGTPTWTSRSPAEENSVTPMQALTNKDDNILFRDSANATSLPVEFGA 360  
 DB 301 GEWSSEPMAGTPTWTSRSPAEENSVTPMQALTNKDDNILFRDSANATSLPVEFGA 360  
 QY 361 G-----LVLGG 366  
 DB 361 SVPLPTFLVAGG 372

RESULT 2  
 IL6RA PIG STANDARD; PRT; 467 AA.  
 AC 018796;  
 DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.  
 DT 01-DEC-2000, sequence version 2.  
 DT 07-MAR-2006, entry version 49.  
 DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)  
 DE (CD126 antigen).  
 GN Name=IL6R; (Pig).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RA Morris K.R., Strom A.D.G.;  
 RT "Cloning and expression of biologically active porcine IL-6 receptor  
 RT alpha chain.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 123-186.  
 RA Klir J.J., Matteri R.L.;  
 RT Partial cDNA sequence of porcine interleukin 6 receptor.";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6  
 CC with low affinity, but does not transduce a signal. Signal  
 CC activation necessitate an association with IL6ST. Activation may  
 CC lead to the regulation of the immune response, acute-phase  
 CC reactions and hematopoiesis.  
 CC -!- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in liver.

CC -!- DOMAIN: The two fibronectin type-III-like domains contained in the  
 CC C-terminal part form together a cytokine-binding domain.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.  
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 CC domain.

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CC EMBL; AF147881; AAF73109.1; -; mRNA.  
 CC EMBL; AF415116; AAB70916.1; -; mRNA.  
 CC HSSP; P08887; IN26.  
 DR SMR; O18796; 20-318.  
 DR InterPro; IPR002996; Cytokn rcpt\_B/G.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR003530; Hempt\_rcpt\_L\_F3.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig C2.  
 DR InterPro; IPR013151; Immunoglobulin.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50853; FN3; 1.  
 DR PROSITE; PS01354; HEMATOPO REC L\_F3; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 19 By similarity.  
 FT CHAIN 20 467 Interleukin-6 receptor alpha chain.  
 FT /FTID=PRO 0000010897.  
 FT Extracellular (Potential).  
 FT Potential.  
 FT TOPO\_DOM 20 365 Potential.  
 FT TRANSMEM 366 386  
 FT TOPO\_DOM 387 467 Cytoplasmic (Potential).  
 FT DOMAIN 20 112 Ig-like C2-type.  
 FT DOMAIN 216 311 Fibronectin type-III.  
 FT MOTIF 303 307 WSXWS motif.  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 221 221 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 25 193 By similarity.  
 FT DISULFID 47 96 By similarity.  
 FT DISULFID 121 132 By similarity.  
 FT DISULFID 165 176 By similarity.  
 SQ SEQUENCE 467 AA; 51067 MW; A2B0B884BF21C502 CRC64;

Query Match 50.5%; Score 1471; DB 1; Length 467;  
 Best Local Similarity 75.5%; Pred. No. 2.7e-98;  
 Matches 281; Conservative 27; Mismatches 58; Indels 6; Gaps 1;  
 QY 1 MLAVGCALLAALAAAPGALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 DB 1 MLAVGCALLAALAAAPGALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
 QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRPAQVTHLLVDVPPPEPOL 120  
 DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSYRAGRPAQVTHLLVDVPPPEPOL 120  
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESKQSCQLAV 180  
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESKQSCQLAV 180  
 QY 181 PEGDSSFFIVSMCVASSVSGSKFSTQTQGGCGILQDPPANITVTAVARNPRLSVTWQD 240  
 DB 181 PEGDSSFFIVSMCVASSVSGSKFSTQTQGGCGILQDPPANITVTAVARNPRLSVTWQD 240

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Qy 241 PHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQBEFG 300
Db 241 PPSNWSFYRLQFLRYRAERSKFTTMMVKELQHCVIHDWGLRHVVQLRAQBEFGH 300
Qy 301 GEMSEWSPAMGTPTWTSRSPAEENEVSTPMQALTTNKDDNIIILFRSANATSLPVEFGA 360
Db 301 GLMSEWQEVGTPTWTSRSPAEETPLSTQAPTNNEDDDISSKESANATSLPVDOSA 360
Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAG 372

RESULT 3
IL6RA RAT
ID IL6RA RAT STANDARD; PRT; 462 AA.
AC P22273,
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 2.
DT 07-MAR-2006, entry version 57.
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=IL6r;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Fischer 344; TISSUE=Liver;
RX MEDLINE=91060602; PubMed=2174054;
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RT rat liver interleukin 6 receptor.";
RL J. Biol. Chem. 265:19853-19862(1990).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA Gibson T.;
RL Unpublished observations (FEB-1995).
CC -!- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitate an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -!- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- DOMAIN: The two fibronectin type-III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: M58587; AAA41431.1; -; mRNA.
CC DR PIR: A37986; A37986.
CC DR HSSP: P08887; IN26.
CC DR Ensembl: ENSRNCG00000020811; Rattus norvegicus.
CC DR RGD: 2902; IL6r.
CC DR InterPro: IPR002996; Cytokn rcpt_B/G.
CC DR InterPro: IPR003961; FN III.
CC DR InterPro: IPR003530; Hempt_rcpt_L_F3.
CC DR InterPro: IPR003599; Ig.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR013151; Immunoglobulin.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00409; IG_1.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS0853; FN3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 19 Interleukin-6 receptor alpha chain.
FT CHAIN 20 462 /FTid=PRO_000010898.
FT FT Extracellular (Potential).
FT FT Potential.
FT FT Cytoplasmic (Potential).
FT FT Ig-like C2-type.
FT FT Fibronectin type-III.
FT FT WSXWS motif.
FT FT MOTIF 300 304 Poly-Pro.
FT FT COMPBIAS 404 408 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 32 32 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 150 150 N-linked (GlcNAc...) (Potential).
FT FT DISULFID 25 190 By similarity.
FT FT DISULFID 47 92 By similarity.
FT FT DISULFID 117 128 By similarity.
FT FT DISULFID 162 173 By similarity.
FT FT DISULFID 227 261 By similarity.
FT FT CONFLICT 262 261 XPRLKVSQWDPFGSDWSYLLQFLRYRPVWSKX -> SL
FT FT VGSKSVGKLTSLPGFTVTCNNSFDLYGORT (in
FT FT Ref. 1).
SQ SEQUENCE 462 AA; 50401 MW; A4D6064CEDC0537D CRC64;

Query Match 34.2%; Score 994.5; DB 1; Length 462;
Best Local Similarity 51.9%; Pred. No. 1.3e-63;
Matches 195; Conservative 50; Mismatches 116; Indels 15; Gaps 5;

Qy 1 MLAVGCALLAALAAAGCAALAPRRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHW 60
Db 1 MLAVGCTLLVALLAAPAVALLVGLSCRALEVANGVTSLPGATVTLICPGKEAGNATIH 60
Qy 61 VLKPAAGSHPSWAGMRLLRSVLHDSGNVSCVCRACRPACTVHLLVDVPEEPOLS 120
Db 61 VY---SGSQSRENTTGTNLVLRVQVNDTHYLCFLDDBHLVGTVPLLDVPEEPKLS 116
Qy 121 CFRKSPLSNVVCEWGPSTSLTTKALLVRKFNQSPAE-DFQEPQCOYSQSKFSCOLA 179
Db 117 CFRKNPLVNAFCEWHPSSTPSPTTKAVMFARKINTNGKSGDFQVPCQYSQQLKSFCEVE 176
Qy 180 VPEGDSFYSVMCMVASSVSGSKFTQTFCGCLQDPDPANITVTAVARNPRWLSVTWQ 239
Db 177 ILEGDKYHIVSLCVANSVGRSSHNVVFSQSLKMWQDPDPANLVSAIPGKPRMLKVSQ 236
Qy 240 DPHSNWSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQBEFG 299
Db 237 DPESWDPSSYYLQFLRYRPVWSKXFTVWPLQVAHQCVIHDALRGVHVQVQKBEFD 296
Qy 300 QGEMSEWSPAMGTPTW-TESRSPAEENEVSTPMQALTTNKDDNIIILFRSANATSL---- 354
Db 297 IGOMSKWSPEVTGTPMLAEPRITTPA-GIPGNPTQVSVEDYDNHEDYQGSSTEATSLVAPV 355
Qy 355 ----PVEFGAGLVLG 366
Db 356 QGSSPIPLPTFLVAG 371

RESULT 4
Q3URV7 MOUSE
ID Q3URV7 MOUSE PRELIMINARY; PRT; 459 AA.
AC Q3URV7;
DT 11-OCT-2005, integrated into UniProtKB/TREMBL.

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DT 11-OCT-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 8.  
 DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,  
 DE clone:C230098M17 product:interleukin 6 receptor, alpha, full insert  
 DE sequence.  
 GN Name=Il6ra;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA Di Bernardo D., Down T., Engstrom P., Fagioli N., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Hummel S., Iacono M., Ikeo K., Iwama T., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsumura S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
 RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,  
 RA Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grummond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grummond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,  
 RA Hirokawa-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1757-1771(2000).  
[8]

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RT NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Arakawa T., Carninci P., Fukuda S., Haehizume W., Hayashida K.,
RA Hori F., Iida J., Inamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Havaehizaki Y.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AK141197; BAE24580.1; -; mRNA.
DR MGI; MGI:105304; Il6ra.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR InterPro; IPR002996; Cyt_kn_rcpt_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 50384 MW; 3575EBFC6AB8477 CRC64;

Query Match 33.1%; Score 963; DB 2; Length 459;
Best Local Similarity 50.9%; Pred. No. 2.4e-61;
Matches 191; Conservative 49; Mismatches 121; Indels 14; Gaps 5;

QY 1 MLAVGCALLAALLAAGPAALAPRCPAQEVARGVLTSLPGDSVTLTCGPVEPEDNATVHW 60
DB 1 MLTVGCTLLVALLAAPAVALVLSGRALVANGVITSLPGATVTLICPGEEAGNVTHW 60
QY 61 VLRKPAAGSHPSRWAGMRRLLLSVLHDSNGVSCYRAGPAGTVHLLVDVPPPEFQLS 120
DB 61 VY-----SGSQNRWTTTNTLVLRDVLQSLDGTGDLCSLNDHLVGTVPLLVDVPPPEPKLS 116
QY 121 CFRKSPLSNVVCEGPRSTPSLTTKAVLLVRKFNQSPAE-DFQEPCCOYSQESQKFSCLA 179
DB 117 CFRKNPLVNAICEWRPSTPSPTTKAVLFAKKINTNGKSDFPVPCQYSSQOLKSFSCQVE 176
QY 180 VPEGDSGFYIVCMCVASSVSGSKFSTOTFOCGILQDPDPANITVTAVARNPRLSVTWQ 239
DB 177 ILEGDKYHIVSLCVANSVSGSKSHNEAFSLKMKVQDPDPANLVVSAIPGRPRLKVSQ 236
QY 240 DPHSWNSFYRLRFLRYAERSKTFTTMMVKDIQHHCVTHDWSGLRHVVQLRAQEFEG 299
DB 237 HPETWDSYLLQLQRLRYRPMVSKFTVLLLPVAQYQCVIHDALRGVKHVQVRGSELD 296
QY 300 QGENSENSPEAKGTPTWETSPRAENSVETPMQALTTNKDDNTILFRDSANATSL--PVE 357
DB 297 LGQENSESPVETGTPWTEPRTTPA-GILWNPQTQSVSDSANHEDQYSSSTEATSVLAPVQ 355
QY 358 FGAG-----LVLAG 366
DB 356 ESSSMSPTEFLVAGG 370

RESULT 5
IL6RA MOUSE
ID IL6RA MOUSE STANDARD; PRT; 460 AA.
AC P22272;
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DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 2.
DT 07-MAR-2006, entry version 60.
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=Il6ra; Synonyms=Il6r;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=90278354; PubMed=2112585; DOI=10.1084/jem.171.6.2001;
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytogenesis.";
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C3H; TISSUE=Liver;
RA Florillo M.T., Ciliberto G., Dente L.;
RA Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitate an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- DOMAIN: The two fibronectin type-III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -1- DOMAIN: The WSWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -----
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CC -----
DR EMBL; X51975; CAA36237.1; -; mRNA.
DR EMBL; X53802; CAA37810.1; -; mRNA.
DR PIR; JLO144; JLO144.
DR PIR; JLO145; JLO145.
DR HSP; P08887; IN26.
DR Ensembl; ENSMUSG0000027947; Mus musculus.
DR MGI; MGI:105304; Il6ra.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002996; Cyt_kn_rcpt_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;
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RT FHCR. Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (JUN-2001) to the ENBL/GenBank/DBJ databases.  
RN [11]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Lung;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.C., Haiech F.,  
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [12]  
RP PROTEIN SEQUENCE OF 30-63.  
RX MEDLINE=8915445; PubMed=3279116;  
RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,  
RA Billiau A.;  
RT "Separation and comparison of two monokines with lymphocyte-activating  
RT factor activity: IL-1 beta and hybridoma growth factor (HGF).  
RT Identification of leukocyte-derived HGF as IL-6.";  
RL J. Immunol. 140:1534-1541 (1988).  
RN [13]  
RP PROTEIN SEQUENCE OF 30-50.  
RX MEDLINE=90121567; PubMed=2610854;  
RA Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;  
RT "Interleukin 6 is the principal cytolytic T lymphocyte differentiation  
RT factor for thymocytes in human leukocyte conditioned medium.";  
RL J. Mol. Cell. Immunol. 4:203-211 (1989).  
RN [14]  
RP PROTEIN SEQUENCE OF 30-40, AND GLYCOSYLATION.  
RX MEDLINE=9135364; PubMed=1893960; DOI=10.1016/1043-4666(91)90018-9;  
RA May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;  
RT "Marked cell-type-specific differences in glycosylation of human  
RT interleukin-6.";  
RL Cytokine 3:204-211 (1991).  
RN [15]  
RP PROTEIN SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE  
RP BOND.  
RX MEDLINE=9515434; PubMed=7851440;  
RA Berton J., la Fiura A., Bertolero F., Orsini G., Valeasina B.,  
RA Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;  
RT "Structure, stability and biological properties of a N-terminally  
RT truncated form of recombinant human interleukin-6 containing a single  
RT disulfide bond.";  
RL Eur. J. Biochem. 227:573-581 (1995).  
RN [16]  
RP DISULFIDE BONDS.  
RX MEDLINE=89286115; PubMed=2472117;  
RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;  
RT "Disulfide structures of human interleukin-6 are similar to those of  
RT human granulocyte colony stimulating factor.";  
RL Arch. Biochem. Biophys. 272:144-151 (1989).  
RN [17]  
RP MUTAGENESIS.  
RX MEDLINE=91243808; PubMed=2037043; DOI=10.1016/0014-5793(91)80491-K;  
RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;  
RT "Evidence for the importance of a positive charge and an alpha-helical  
RT structure of the C-terminus for biological activity of human IL-6.";  
RL FEBS Lett. 282:265-267 (1991).

4  
RN [18]  
RP STRUCTURE BY NMR.  
RX MEDLINE=96134845; PubMed=8555185; DOI=10.1021/bi951949e;  
RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;  
RT "Folding topologies of human interleukin-6 and its mutants as studied  
RT by NMR spectroscopy.";  
RL Biochemistry 35:273-281 (1996).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933;  
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,  
RA Cumming D.A.;  
RT "Solution structure of recombinant human interleukin-6.";  
RL J. Mol. Biol. 268:468-481 (1997).  
RN [20]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;  
RA Somers W., Stahl M., Seehra J.S.;  
RT "1.9-A crystal structure of interleukin 6: implications for a novel  
RT mode of receptor dimerization and signaling.";  
RL EMBO J. 16:989-997 (1997).  
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological  
CC functions: it plays an essential role in the final differentiation  
CC of B-cells into Ig-secreting cells, it induces myeloma and  
CC plasmacytoma growth, it induces nerve cells differentiation, in  
CC hepatocytes it induces acute phase reactants.  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- PTM: N- and O-glycosylated.  
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.  
CC -!- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL6;  
CC WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyId=208".  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; X04430; CAA28026.1; -; mRNA.  
DR EMBL; M14584; AAA52728.1; -; mRNA.  
Query Match 32.5%; Score 947.5; DB 1; Length 212;  
Best Local Similarity 95.0%; Pred. No. 1.2e-60;  
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;  
QY 355 PVSEFGAG--LVIGQGF-MPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIALRKE 411  
Db 11 PVAFSLGLLLVLPAAFPAPVPPEGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIALRKE 70  
QY 412 TCNKSNNCESSKEALAENNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQ 471  
Db 71 TCNKSNNCESSKEALAENNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQ 130  
QY 472 NRFESEBEQARAVQMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMT 531  
Db 131 NRFESEBEQARAVQMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMT 190  
QY 532 THILRSFKFLOSSLRALRQM 553  
Db 191 THILRSFKFLOSSLRALRQM 212  
RESULT 7  
Q75MH2\_HUMAN  
ID Q75MH2\_HUMAN PRELIMINARY; PRT; 212 AA.  
AC Q75MH2;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 21-FEB-2006, entry version 7.  
DE Hypothetical protein IL6 (Interleukin 6) (Interferon, beta 2).  
GN Name=IL6;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22737599; PubMed=12853948; DOI=10.1038/nature01782;  
 RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
 RA Wagner-McPherson C., Layman D.C., Maas J., Jaeger S., Walker R.,  
 RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
 RA Fowell G.A., Delehaunt K.D., Miner T.L., Nash W.E., Cordes M., Du H.,  
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J.J., Andrews S., Isak A.,  
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,  
 RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strommatt C.,  
 RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,  
 RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,  
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,  
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,  
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,  
 RA Simms E., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,  
 RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,  
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,  
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
 RA Waterston R.H., Wilson R.K.;  
 RT "The DNA sequence of human chromosome 7";  
 RL Nature 424:157-164(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Haekenson W., Nguyen C., Yeakum M.;  
 RT "The sequence of Homo sapiens BAC clone RP11-240H8.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Waterston R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wilson R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor  
 RT vector.";  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; AC073072; AAS07539.1; -; Genomic DNA.  
 DR EMBL; BT019748; AAV38553.1; -; mRNA.  
 DR EMBL; BT019749; AAV38554.1; -; mRNA.  
 DR EMBL; CR450296; CAG29292.1; -; mRNA.  
 DR SMR; Q75MH2; 47-212.  
 DR Ensembl; ENSG00000136244; Homo sapiens.  
 DR GO; GO:0005615; C:extracellular space; ISS.  
 DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.  
 DR GO; GO:0007267; P:cell-cell signaling; ISS.  
 DR GO; GO:0006959; P:humoral immune response; ISS.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.  
 DR InterPro; IPR012351; Cytokine\_4\_hlx.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR InterPro; IPR003574; Interleukin\_6.  
 DR PANTHER; PTHR11457; Interleukin\_6; 1.  
 DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.  
 DR PRINTS; PR00434; INTERLEUKIN\_6.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 212 AA; 23718 MW; 1FIEDIFE1B734079 CRC64;  
 Query Match 32.5%; Score 947.5; DB 2; Length 212;  
 Best Local Similarity 95.0%; Pred. NO. 1.2e-60;  
 Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;  
 QY 355 PVEFGAG--IVLGQGF-MPVPPGDSKDVAAAPHRQPLTSSSRIDKQIRVILDGISALRKE 411  
 DB 11 PVAFSLGULLVLPAAFPAPVPVPGDSKDVAAAPHRQPLTSSSRIDKQIRVILDGISALRKE 70  
 QY 412 TCNKSNMCESSKEALAEANNLNLPMWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEVLIQ 471  
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 QY 472 NRPESSEQARAVQMSKVLQIFLOKKAINDAITTPDPTTNASLLTKLAQNQLQDMT 531  
 DB 131 NRPESSEQARAVQMSKVLQIFLOKKAINDAITTPDPTTNASLLTKLAQNQLQDMT 190  
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 DB 191 THILRSKPEFLQSSLRALRQM 212  
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 AC P79341;  
 ID IL6 MACFA  
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAY-1997, sequence version 1.  
 DT 07-FEB-2006, entry version 35.  
 DE Interleukin-6 precursor (IL-6).  
 GN Name=IL6;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheidae; Cercopithecinae; Macaca.  
 OX NCBI\_taxid=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RA Tateumi M.;  
 RT "Molecular cloning and expression of cynomolgus monkey interleukin-  
 RT 6.";  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological  
 CC functions: it plays an essential role in the final differentiation  
 CC of B-cells into Ig-secreting cells, it induces myeloma and  
 CC plasmacytoma growth, it induces nerve cells differentiation, in  
 CC hepatocytes it induces acute phase reactants (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted protein.  
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.  
 CC  
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 DR EMBL; AB000554; BAA19148.1; -; mRNA.  
 DR HSSP; P05231; IL6.  
 DR SMR; P79341; 47-212.  
 DR InterPro; IPR012351; Cytokine\_4\_hlx.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
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 DR PANTHER; PTHR11457; Interleukin\_6; 1.  
 DR Pfam; PF00489; IL6; 1.  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR PRINTS; PR00434; INTERLEUKIN\_6.  
 DR ProDom; PD004356; Interleukin\_6; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.

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FT SIGNAL 1 27 Potential.
FT CHAIN 28 212 Interleukin-6.
FT CARBOHYD 73 73 /FTid=PRO.0000015584.
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FT DISULFID 72 78 N-linked (GlcNAc...) (Potential).
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF080389 CRC64;

Query Match 31.5%; Score 916.5; DB 1; Length 212;
Best Local Similarity 92.1%; Pred. No. 2.1e-58;
Matches 186; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVGGQF-MPVPPGDSKDVAAPHQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSLGLLLVLPAAFPAPVLPVPGDSKDVAAPHQPLTSSERIDKHIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKQCGFQSGFNEETCLVKIITGLLEFEVYLYLQ 471
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Db 191 THILRSFKFQSSLRALRQM 212

RESULT 9
IL6_MACTH STANDARD; PRT; 212 AA.
AC Q5I6E3;
DT 12-APR-2005, integrated into UniProtKB/Swiss-Prot.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca thibetana (Pere David's macaque) (Tibetan macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=54602;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Wei K., Zou F.D., Xia S., Pan J., Yue B.S.;
RT "Molecular cloning and characterization of the interleukin 6 (IL6) gene from Tibetan macaque (Macaca thibetana) and its expression in Escherichia coli.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
EMBL; AY849928; AA033962.1; -; mRNA.
DR SMR; Q5I6E3; 47-212.
DR InterPro; IPR012351; IL6_MGF_GCSF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
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DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 212 Interleukin-6.
FT CARBOHYD 73 73 /FTid=PRO.0000015586.
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 N-linked (GlcNAc...) (Potential).
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23626 MW; D0916CF3AF0B039E CRC64;

Query Match 31.3%; Score 912.5; DB 1; Length 212;
Best Local Similarity 91.6%; Pred. No. 4.1e-58;
Matches 185; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVGGQF-MPVPPGDSKDVAAPHQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSLGLLLVLPAAFPAPVLPVPGDSKDVAAPHQPLTSSERIDKHIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKQCGFQSGFNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNRSNNCESSKEALAENNLNPKMAEKQCGFQSGFNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRFESEBEQARAVQMSKVLQIQLQKAKNLDAITTPDTTNASLLTKLQANQWLODMT 531
Db 131 NRFESEBEQARAVQMSKVLQIQLQKAKNLDAITTPDTTNASLLTKLQANQWLODMT 190
Qy 532 THILRSFKFQSSLRALRQM 553
Db 191 THILRSFKFQSSLRALRQM 212

RESULT 10
IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 35.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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EMBL; L26028; AAA99978.1; -; mRNA.
DR HSPSP; P05231; IALU.
DR SMR; P51494; 47-212.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
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DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 212 Interleukin-6.
FT CARBOHYD 73 73 /FTID=PRO 0000015585.
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 N-linked (GlcNAc...) (Potential).
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCAD CRC64;

Query Match 31.2%; Score 908.5; DB 1; Length 212;
Best Local Similarity 91.1%; Pred. No. 7.9e-58;
Matches 184; Conservative 5; Mismatches 10; Indels 3; Gaps 2;

QY 355 PVEFGAG--LVLGQGF-MPVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 411
DB 11 PVAFSLGLLLVLPAPFAPVLPVGGDSKNVAAPHSQPLTSSERIDKHIRYILDGIALRKE 70

QY 412 TCNKNMCESSKEALAENNLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEPEVYLEYIQ 471
DB 71 TCNRSNMCESSKEALAENNLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEPEVYLEYIQ 130

QY 472 NRPESSEQARAVQSTKVLIOFLQKAKNLDATITPPTTNASLLTKLQAOQNQLQDMT 531
DB 131 NRPESSEQARAVQSTKVLIOFLQKAKNLDATITPPTTNASLLTKLQAOQNQLQDMT 190

QY 532 THILRSFKFLOSLRALQRM 553
DB 191 THILRSFKFLOSLRALQRM 212

RESULT 11
O97540 AOTNA PRELIMINARY; PRT; 209 AA.
AC O97540;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DE 21-FEB-2006, entry version 25.
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]_TaxID=37293;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey";
RL Immunogenetics 54:645-653(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC
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CC
CC -----
CC EMBL; AF014510; AAD01536.1; -; mRNA.
CC HSSP; P05231; 1ALU.
CC SMR; O97540; 47-209.
CC GO; GO:0005615; C:extracellular space; ISS.
CC GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
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DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0006959; P:humoral immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase.
FT NON_TER 1 1
FT NON_TER 209 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 31.2%; Score 907.5; DB 2; Length 209;
Best Local Similarity 92.0%; Pred. No. 9.2e-58;
Matches 183; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 355 PVEFGAG--LVLGQGF-MPVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 411
DB 11 PVAFSLGLLLVMPAPFAPVPPGDSKEVAAPNROPLTSTEQIDKHIRYILDGIALRKE 70

QY 412 TCNKNMCESSKEALAENNLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEPEVYLEYIQ 471
DB 71 TCNKNMCESSKEALAENNLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEPEVYLEYIQ 130

QY 472 NRPESSEQARAVQSTKVLIOFLQKAKNLDATITPPTTNASLLTKLQAOQNQLQDMT 531
DB 131 NRPESSEQARAVQSTKVLIOFLQKAKNLDATITPPTTNASLLTKLQAOQNQLQDMT 190

QY 532 THILRSFKFLOSLRAL 550
DB 191 THILRSFKFLOSLRAL 209

RESULT 12
IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=Fuj;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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CC
CC -----
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DR EMBL; L26032; AAA99972.1; -; mRNA.
DR HSP; P05231; IALU.
DR SMR; P46650; 47-212.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 31.1%; Score 904.5; DB 1; Length 212;
Best Local Similarity 90.6%; Pred. No. 1.6e-57;
Matches 183; Conservative 5; Mismatches 11; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 411
Db 11 PVAFSLGLLLVPAAPFAPVLPVPGDSKDVAAPHSQPLTSSERIDKHIRYILDGIALRKE 70

Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYQ 471
Db 71 TCNRSNNCDSTKEALAENNLNPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYQ 130

Qy 472 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQWLODMT 531
Db 131 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQWLODMT 190

Qy 532 THILRSFKFQSSSLRALRQM 553
Db 191 THILRSFKFQSSSLRALRQM 212

RESULT 13
IL6_SAISC
AC OBMKH0;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
OX NCBI_TaxID=9521;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA Heraud J.M., Lavergne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel
RL monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RC Immunogenetics 54:20-29(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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DR EMBL; AF294757; AAK92044.1; -; mRNA.
DR HSP; P05231; IL6.
DR SMR; OBMKH0; 47-212.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;

Query Match 27.8%; Score 810.5; DB 1; Length 212;
Best Local Similarity 83.2%; Pred. No. 1.1e-50;
Matches 168; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 411
Db 11 PVAFSLGLLLVPAAPFAPVLPVPGDSKEVAAPRQLTSTERIDKHIWYILDGIALRKE 70

Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYQ 471
Db 71 ICNKSNNCESSKEALAENNLNPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYQ 130

Qy 472 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQWLODMT 531
Db 131 NREFSSEQARAVQMSTKGLIQSLQKAKNLDAITPDATNASLLTKLAQDQWLOQVT 190

Qy 532 THILRSFKFQSSSLRALRQM 553
Db 191 THILRSFKFQSSSLRALRQM 212

RESULT 14
Q91TH3_AOTLE
ID Q91TH3_AOTLE PRELIMINARY; PRT; 209 AA.
AC Q91TH3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE Interleukin-6 (fragment).
GN Name=IL-6;
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aotinae; Aotus.
OX NCBI_TaxID=43147;
[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey.";
RC Immunogenetics 54:645-653(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and

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CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC
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CC
CC EMBL; AF097323; AAF21298.1; -; mRNA.
CC HSSP; P05231; 1ALU.
CC SMR; Q9TH3; 47-209.
CC GO; GO:0005615; C:extracellular space; ISS.
CC GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
CC GO; GO:0007267; P:cell-cell signaling; ISS.
CC GO; GO:0006959; P:humoral immune response; ISS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
CC GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC PANTHER; PTHR11457; Interleukin_6; 1.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC ProDom; PD004356; Interleukin_6; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Acute phase.
CC NON_TER 1
CC NON_TER 209
CC NON_TER 209 AA; 23116 MW; AOA3DFAA4BF560CC CRC64;
CC SEQUENCE 209 AA; 23116 MW; AOA3DFAA4BF560CC CRC64;
CC
CC Query Match 27.8%; Score 808.5; DB 2; Length 209;
CC Best Local Similarity 83.9%; Pred. No. 1.5e-50;
CC Matches 167; Conservative 10; Mismatches 19; Indels 3; Gaps 2;
CC
CC QY 355 PVEFGAG--LVLGGQF-MPVPPGDSKDVAAPHROPLTSERIDKQIRYILDGIALRKE 411
CC Db 11 PVAFSLGLLVMPAPFAPVPLGDSKEVAPNRLTSTEQIDKHRYILEGISALRKE 70
CC
CC QY 412 TCKNSNMCSSEKEALAEANLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEFEVLEYIQ 471
CC Db 71 ICDKSNMCSSEKEALAEANLNLPKMAEKDGGCFQSGFNEETCLVKIITGLLEFEVLEYIQ 130
CC
CC QY 472 NRFESSEQAGAVQSTKVLQFTLQKKAKNLDATTPDPTTNASLLTKLQACNQLQDWT 531
CC Db 131 NRFESSEQAGAVQSTKGLIQLQSKAKNLSAIAITPDNATNLSLMLKQADQLQGV 190
CC
CC QY 532 THLILRSFKFQLQSLRAL 550
CC Db 191 THLILRSFKFQLQSLRAL 209
CC
CC RESULT 15
CC Q5DW05 CHICK
CC ID Q5DW05_CHICK PRELIMINARY; PRT; 445 AA.
CC AC Q5DW05;
CC DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
CC DT 29-MAR-2005, sequence version 1.
CC DT 07-MAR-2006, entry version 8.
CC DE Interleukin-6 receptor alpha chain precursor.
CC GN Name=il6ra;
CC OS Gallus gallus (Chicken).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE.
CC RX PubMed=16153708; DOI=10.1016/j.j.dci.2005.05.007;
CC RA Nishimichi N., Kawashima T., Hojo S., Horiuchi H., Furusawa S.,
CC RA Matsuda H.;
CC RT "Characterization and expression analysis of a chicken interleukin-6
CC receptor alpha."
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RL Dev. Comp. Immunol. 30:419-429(2006).
CC -|- SUBUNIT: Heterotrimer of the alpha chain, LIPR and IL6ST (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -|- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
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CC
CC EMBL; AB175664; BA090557.1; -; mRNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC InterPro; IPR002996; Cytokn rcpt_B/G.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003530; Hempt_rcpt_L_F3.
CC InterPro; IPR003599; IG.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR013151; Immunoglobulin.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00060; FN3; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS0853; FN3; 1.
CC PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
CC PROSITE; PS0835; IG_Like; 1.
CC Immunoglobulin domain; Membrane; Receptor; Repeat; Signal;
CC SIGNAL 1 20 Potential.
CC CHAIN 21 445 Potential.
CC SEQUENCE 445 AA; 48827 MW; BIA90D89BD2776D9 CRC64;
CC
CC Query Match 23.0%; Score 670; DB 2; Length 445;
CC Best Local Similarity 41.0%; Pred. No. 4.8e-40;
CC Matches 159; Conservative 51; Mismatches 118; Indels 60; Gaps 12;
CC
CC QY 8 LLAALLAAGGAALAP-RCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLRKA 66
CC Db 8 LRAALLLTAAASSAPRRRCGPVALPQDTVLGRPGANVTLCCRREP-PNGTVLWSGRRRA 66
CC
CC QY 67 AGHPSRWAGMRILLRLSLVHDSGNYSVCYRACRAGTCTVLLVDVPPPEPOLSCFRKSP 126
CC Db 67 LGG-----GNALLGLRPEDAGRYSCHLGHGHTLVLLVEEPPEPHVSCSRSH 118
CC
CC QY 127 LSNVVCWGPRTSLTTKAVL-LVRKFNQSPAEQFQPCQYSQBSQKFCOLAYPEG-- 183
CC Db 119 DKDVLCEWRPRASAPGTRAVLWMKRFTMENAT--EQCHFYSAQKFCVKVPPGTD 176
CC
CC QY 184 DSSFYIVSMCVASSVSGSKFSTQTFQGGIILQOPPPANITVTAVARNRWLSVTWQDPHS 243
CC Db 177 DTKALVWSVCVSSRAGSAAEDRIFTLNGILKDPPLNVTVEAVERSPQLCVRWSYPPS 236
CC
CC QY 244 WNSSFYRLRFLRYRAERSKFTT-----TMMVKDLQHCCHVDHAWGLRHVQLRAQE 296
CC Db 237 WDPFYRLRFQVRYRPEPAPNFTQVDQVTRTWL-----DIRDAWGRMHVVQVRAQE 288
CC
CC QY 297 EFGQSEWSEWSPAMGTPTWTSRSPPAENESTPMQALTNNKDDNILFRSANATSLPV 356
CC Db 289 EFGHGANSREAVGTPWTFRDVTENGLSYSSQFPA-----EDD-----PY 330
CC
CC QY 357 EFGAGLVLGQGFMPVPP---GEDSKDVA 381
CC Db 331 GYGATL-----PPELFGDDTADDA 349
CC
CC Search completed: September 7, 2006, 23:03:01
CC Job time : 304 secs
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10/11/18

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 23:03:15 ; Search time 49 Seconds  
(without alignments)  
987.846 Million cell updates/sec

Title: US-09-462-416A-13  
Perfect score: 2912  
Sequence: 1 MLVGCALLAALLAAPGAAL.....LILSRKFELQSSLRALROM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pdp.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pdp.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pdp.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pdp.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCUS\_COMB.pdp.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pdp.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1927.5	66.2	592	2	US-09-313-942-8
2	1927.5	66.2	592	2	US-10-282-162-8
3	1917	65.8	468	2	US-08-795-473B-5
4	1917	65.8	468	2	US-09-439-856-5
5	1917	65.8	468	2	US-09-949-016-5959
6	1917	65.8	468	7	5171840-2
7	1917	65.8	468	7	5480796-2
8	1910	65.6	360	2	US-09-313-942-15
9	1910	65.6	360	2	US-10-282-162-15
10	1852	63.6	344	7	5171840-7
11	1852	63.6	344	7	5480796-7
12	1789	61.4	1158	2	US-09-313-942-26
13	1789	61.4	1158	2	US-10-282-162-26
14	1783	61.2	1168	2	US-09-313-942-24
15	1783	61.2	1168	2	US-10-282-162-24
16	1741	59.8	323	7	5171840-6
17	1741	59.8	323	7	5480796-6
18	1683	57.8	315	2	US-09-313-942-16
19	1683	57.8	315	2	US-10-282-162-16
20	1479	50.8	388	2	US-09-949-016-9852
21	1388	47.7	386	7	5171840-5
22	1388	47.7	386	7	5480796-5
23	1153	39.6	210	2	US-09-043-785-1
24	951.5	32.2	232	2	US-09-949-016-10315
25	950	32.6	201	7	5171840-11
26	947.5	32.5	212	1	US-08-792-019B-9

27	947.5	32.5	212	2	US-08-988-819-9	Sequence 9, Appli
28	947.5	32.5	212	2	US-09-016-534-9	Sequence 9, Appli
29	947.5	32.5	212	2	US-08-097-869-7	Sequence 7, Appli
30	947.5	32.5	212	2	US-08-795-473B-6	Sequence 6, Appli
31	947.5	32.5	212	2	US-09-230-637-45	Sequence 45, Appli
32	947.5	32.5	212	2	US-09-230-371A-27	Sequence 27, Appli
33	947.5	32.5	212	2	US-09-439-856-6	Sequence 6, Appli
34	947.5	32.5	212	2	US-09-462-941-13	Sequence 13, Appli
35	947.5	32.5	212	7	5510472-2	Patent No. 5510472
36	945	32.5	317	2	US-08-469-318-145	Sequence 145, App
37	945	32.5	317	2	US-08-468-609A-145	Sequence 145, App
38	945	32.5	317	2	US-08-446-872A-145	Sequence 145, App
39	945	32.5	317	2	US-08-762-227A-145	Sequence 145, App
40	945	32.5	317	5	PCT-US95-01185-145	Sequence 145, App
41	939.5	32.3	212	2	US-09-487-792-14	Sequence 14, Appli
42	939.5	32.3	212	2	US-09-908-594-14	Sequence 14, Appli
43	939	32.2	185	1	US-08-716-317-7	Sequence 7, Appli
44	934	32.1	184	1	US-08-567-047-2	Sequence 2, Appli
45	934	32.1	184	1	US-08-567-048-2	Sequence 2, Appli

## ALIGNMENTS

4

RESULT 1  
US-09-313-942-8  
; Sequence 8, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-8

Query Match		66.2%;	Score 1927.5;	DB 2;	Length 592;
Best Local Similarity		72.8%;	Pred. No. 6.9e-162;		
Matches 391;		Conservative 17;	Mismatches 56;	Indels 73;	Gaps 8;
Qy	1	MLVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLT	CGVVEPEDNATVHW	60	
Db	1	MVAVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLT	CGVVEPEDNATVHW	60	
Qy	61	VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNISYCRAGRPAAGT	VHLLVDVPPPEPQLS	120	
Db	61	VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNISYCRAGRPAAGT	VHLLVDVPPPEPQLS	120	
Qy	121	CFKXSPLSNVVCEWGRPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQY	SOESQKFSQCLAV	180	
Db	121	CFKXSPLSNVVCEWGRPRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQY	SOESQKFSQCLAV	180	
Qy	181	PEGSSFFIIVSMCVASSVSGSKFKSTQTFQGGCILOPDPDPPANTIT	TVAVARNRWLSVTWOD	240	
Db	181	PEGSSFFIIVSMCVASSVSGSKFKSTQTFQGGCILOPDPDPPANTIT	TVAVARNRWLSVTWOD	240	
Qy	241	PHSWNSSFYRLRFELRYAERSKTFITWVMDLQHCVHDAWSGLRHVVQL	RAQBEFQ 300		
Db	241	PHSWNSSFYRLRFELRYAERSKTFITWVMDLQHCVHDAWSGLRHVVQL	RAQBEFQ 300		
Qy	301	GEWSEWSEPAWGTPTWTSRSPPAENESTPQWALTNNKDDNILFRDSANATSL	PVEFG- 359		
Db	301	GEWSEWSEPAWGTPTWTSRSPPAENESTPQWALTNNKDDNILFRDSANATSL	PVEFG- 359		

Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG 360  
Qy 360 -----AGLVLGQ-----FMPVPPGSDSKDVAAPHRQPL-----TSSER 393  
Db 361 EPKSCDKTHTCPAPAPELLGGSPSVFLPPKP-----KDTLMISRTPEVTCVVVDVSHED 415  
Qy 394 IDKQIRYILDGI-----SALRKETCNKNCESSKEALAENNLN-----LPK 435  
Db 416 PEVKFNWVDGVEVHNAKTKPREQYNSYRVSVLTVLHQDWLNGKEYKCKVSNKALPA 475  
Qy 436 MAEKDGCFCQSGFNEE-----TCLVKITGLLLEFVEVLYQLON 472  
Db 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEMESN 529

RESULT 2  
US-10-282-162-8  
; Sequence 8, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282.162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-8

Query Match 66.2%; Score 1927.5; DB 2; Length 592;  
Best Local Similarity 72.8%; Pred. No. 6.9e-162;  
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;  
Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60  
Db 1 MVAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTGVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTGVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFKQNSPAEDFQPCQYSQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFKQNSPAEDFQPCQYSQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNPRLVSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNPRLVSVTWQD 240  
Qy 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300  
Db 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300  
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVFEG- 359  
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG 360  
Qy 360 -----AGLVLGQ-----FMPVPPGSDSKDVAAPHRQPL-----TSSER 393  
Db 361 EPKSCDKTHTCPAPAPELLGGSPSVFLPPKP-----KDTLMISRTPEVTCVVVDVSHED 415  
Qy 394 IDKQIRYILDGI-----SALRKETCNKNCESSKEALAENNLN-----LPK 435  
Db 416 PEVKFNWVDGVEVHNAKTKPREQYNSYRVSVLTVLHQDWLNGKEYKCKVSNKALPA 475

Qy 436 MAEKDGCFCQSGFNEE-----TCLVKITGLLLEFVEVLYQLON 472  
Db 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEMESN 529

RESULT 3  
US-08-795-473B-5  
; Sequence 5, Application US/08795473B  
; Patent No. 6217858  
; GENERAL INFORMATION:  
; APPLICANT: Galun, Eithan  
; APPLICANT: Nahot, Orit  
; APPLICANT: Blum, Herbert E.  
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating  
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Davidson, Davidson and Kappel, LLC  
; STREET: 1140 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS-DOS EDITOR  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795.473B  
; FILING DATE: 11-FEB-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Davidson, Clifford M.  
; REGISTRATION NUMBER: 32,728  
; REFERENCE/DOCKET NUMBER: 963.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)-997-1028  
; TELEFAX: (212)-997-1037  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
US-08-795-473B-5

Query Match 65.8%; Score 1917; DB 2; Length 468;  
Best Local Similarity 96.8%; Pred. No. 4.1e-161;  
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;  
Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60  
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTGVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTGVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFKQNSPAEDFQPCQYSQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFKQNSPAEDFQPCQYSQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNPRLVSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNPRLVSVTWQD 240  
Qy 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300  
Db 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300  
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVFEGA 360

Db 301 GEWSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVGG 366

Db 361 SVPLPTFLVAGG 372

## RESULT 4

US-09-439-856-5

; Sequence 5, Application US/09439856

; Patent No. 6410009

; GENERAL INFORMATION:

; APPLICANT: Galun, Eithan

; APPLICANT: Nahot, Orit

; APPLICANT: Blum, Herbert E.

; TITLE OF INVENTION: A Pharmaceutical Composition for Treating

; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Davidson, Davidson and Kappel, LLC

; STREET: 1140 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS-DOS EDITOR

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/439,856

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,473

; FILING DATE: 11-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Davidson, Clifford M.

; REGISTRATION NUMBER: 32,728

; REFERENCE/DOCKET NUMBER: 963.1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)-997-1028

; TELEFAX: (212)-997-1037

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 468 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

US-09-439-856-5

Query Match 65.8%; Score 1917; DB 2; Length 468;

Best Local Similarity 96.8%; Pred. No. 4.1e-161;

Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFIVSMCVASSVGSFKSTQTQGGCIGLOPDPANITVTAVARNPRLSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVGSFKSTQTQGGCIGLOPDPANITVTAVARNPRLSVTWOD 240

QY 241 PHSMNSSFYRLRFELRYAERSKTFTTWMVKDQHHCVIHDWSGLRHVVQVQRAQEFQ 300

Db 241 PHSMNSSFYRLRFELRYAERSKTFTTWMVKDQHHCVIHDWSGLRHVVQVQRAQEFQ 300

QY 301 \*GEWSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVEFGA 360

Db 301 GEWSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVGG 366

Db 361 SVPLPTFLVAGG 372

## RESULT 5

US-09-949-016-5959

; Sequence 5959, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5959

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-5959

Query Match

Best Local Similarity 65.8%; Score 1917; DB 2; Length 468;

Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFIVSMCVASSVGSFKSTQTQGGCIGLOPDPANITVTAVARNPRLSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVGSFKSTQTQGGCIGLOPDPANITVTAVARNPRLSVTWOD 240

QY 241 PHSMNSSFYRLRFELRYAERSKTFTTWMVKDQHHCVIHDWSGLRHVVQVQRAQEFQ 300

Db 241 PHSMNSSFYRLRFELRYAERSKTFTTWMVKDQHHCVIHDWSGLRHVVQVQRAQEFQ 300

QY 301 GEWSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVEFGA 360

Db 301 GEWSEWSPAMGTPWTESSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVGG 366

Db 361 SVPLPTFLVAGG 372

## RESULT 6

5171840-2

; Patent No. 5171840

; APPLICANT: KISHIMOTO, TADAMITSU

```
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
; LENGTH: 468
5171840-2

Query Match      65.8%; Score 1917; DB 7; Length 468;
Best Local Similarity 96.8%; Pred. No. 4.1e-161;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300

Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDSS 360
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDSS 360

Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372
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RESULT 7
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
; LENGTH: 468
5480796-2

Query Match      65.8%; Score 1917; DB 7; Length 468;
Best Local Similarity 96.8%; Pred. No. 4.1e-161;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
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Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDSS 360
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDSS 360
Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372

RESULT 8
US-09-313-942-15
; Sequence 15, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-15
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Query Match      65.6%; Score 1910; DB 2; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRPFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 9
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US-10-282-162-15  
; Sequence 15, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-282-162-15

Query Match 65.6%; Score 1910; DB 2; Length 360;  
Best Local Similarity 99.4%; Pred. No. 1.1e-160;  
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
DB 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
QY 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344  
DB 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344

RESULT 10  
5171840-7  
; Patent No. 5171840  
; APPLICANT: KISHIMOTO, TADAMITSU  
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL  
; STIMULATORY FACTOR-2  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/298,694  
; FILING DATE: 19-JAN-1989  
; SEQ ID NO: 7;  
; LENGTH: 344  
5171840-7

Query Match 63.6%; Score 1852; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
DB 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
QY 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344  
DB 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344

RESULT 11  
5480796-7  
; Patent No. 5480796  
; APPLICANT: KISHIMOTO, TADAMITSU  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN  
; FOR HUMAN B CELL STIMULATORY FACTOR-2  
; NUMBER OF SEQUENCES: 8  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/907,650  
; FILING DATE: 02-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 298,694  
; FILING DATE: 19-JAN-1989  
; SEQ ID NO: 7;  
; LENGTH: 344  
5480796-7

Query Match 63.6%; Score 1852; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
DB 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60  
QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120  
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180  
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIIQDPDPANITVTAVARNRWLSVTWQD 240  
QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
DB 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQEEFQ 300  
QY 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344  
DB 301 GEWSWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDDDNIL 344

RESULT 12  
US-09-313-942-26  
; Sequence 26, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

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; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

Query Match      61.4%; Score 1789; DB 2; Length 1158;
Best Local Similarity 58.7%; Pred. No. 3.7e-149; Indels 144; Gaps 13;
Matches 379; Conservative 35; Mismatches 88;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEDEFQPCQYSOESQKSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEDEFQPCQYSOESQKSCQLAV 180
Qy 181 PEGDSSFFIIVSMCVASSVGSFKSTQTQFGCGILQPPDPANITVAVARNRWLSVTWQD 240
Db 181 PEGDSSFFIIVSMCVASSVGSFKSTQTQFGCGILQPPDPANITVAVARNRWLSVTWQD 240
Qy 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDAMSLRHVQLRAQEBFGQ 300
Db 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDAMSLRHVQLRAQEBFGQ 300
Qy 301 GEWSEWSPGAMGTPTWESRSPAEENEVSTPMQAL----- 334
Db 301 GEWSEWSPGAMGTPTWESRSPAEENEVSTPMQAL----- 334
Qy 335 -----TTNKDDNILFRDSANAT-----SLPVEFGAGLVLGQGF 368
Db 361 EKCMQDYFHNANYIVKTNHFTIPKEQYTIINRTASSVTFTDIAASLNILTCNLTFGQL 420
Qy 369 MPVPPGEDSKDVAAPHROPLTSERIDKQIRYILDGIALRKE-----TC-----NKSNNC 419
Db 421 -----EQNVYGITIISGLPPEKPKNLSCTIVNEGKQKRC 453
Qy 420 E--SSKEALAEENLNLPK-----MAEKD---GC-----FOSGFNEETCL 453
Db 454 EWDGGRTHLETNFTLKSEWATHKPADCKAKRDTPTSCVDYSTVYFVNIWVWEAENAL 513
Qy 454 VKIITGLLEFEVYLEYLNQ-----RPFESSEQAARAVQMS-----TKVLIQFIQK 497
Db 514 GKVTSDHINFDPVYKVPKPNPHNLSVINSEBLSILKLTWTNPSIKSVIILKYNIQYRTK 573
Qy 498 KAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEL 543
Db 574 DASTWSQIPPEDTASTRSFT-----VQD-----LKPFTTEYV 605
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RESULT 13
US-10-282-162-26
; Sequence 26, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
```

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; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-26

Query Match      61.4%; Score 1789; DB 2; Length 1158;
Best Local Similarity 58.7%; Pred. No. 3.7e-149; Indels 144; Gaps 13;
Matches 379; Conservative 35; Mismatches 88;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEDEFQPCQYSOESQKSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEDEFQPCQYSOESQKSCQLAV 180
Qy 181 PEGDSSFFIIVSMCVASSVGSFKSTQTQFGCGILQPPDPANITVAVARNRWLSVTWQD 240
Db 181 PEGDSSFFIIVSMCVASSVGSFKSTQTQFGCGILQPPDPANITVAVARNRWLSVTWQD 240
Qy 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDAMSLRHVQLRAQEBFGQ 300
Db 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDAMSLRHVQLRAQEBFGQ 300
Qy 301 GEWSEWSPGAMGTPTWESRSPAEENEVSTPMQAL----- 334
Db 301 GEWSEWSPGAMGTPTWESRSPAEENEVSTPMQAL----- 334
Qy 335 -----TTNKDDNILFRDSANAT-----SLPVEFGAGLVLGQGF 368
Db 361 EKCMQDYFHNANYIVKTNHFTIPKEQYTIINRTASSVTFTDIAASLNILTCNLTFGQL 420
Qy 369 MPVPPGEDSKDVAAPHROPLTSERIDKQIRYILDGIALRKE-----TC-----NKSNNC 419
Db 421 -----EQNVYGITIISGLPPEKPKNLSCTIVNEGKQKRC 453
Qy 420 E--SSKEALAEENLNLPK-----MAEKD---GC-----FOSGFNEETCL 453
Db 454 EWDGGRTHLETNFTLKSEWATHKPADCKAKRDTPTSCVDYSTVYFVNIWVWEAENAL 513
Qy 454 VKIITGLLEFEVYLEYLNQ-----RPFESSEQAARAVQMS-----TKVLIQFIQK 497
Db 514 GKVTSDHINFDPVYKVPKPNPHNLSVINSEBLSILKLTWTNPSIKSVIILKYNIQYRTK 573
Qy 498 KAKNLDAITTPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEL 543
Db 574 DASTWSQIPPEDTASTRSFT-----VQD-----LKPFTTEYV 605
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RESULT 14
US-09-313-942-24
; Sequence 24, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
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Query	1	MLAVGCALLAALLAAPCAALAPRRCPAQEVARGVLTSLPGDVSVTILTCPCGVPEPNATVHM	60
FILE REFERENCE:	REG 203-A		
CURRENT APPLICATION NUMBER:	US/09/313,942		
CURRENT FILING DATE:	1999-05-19		
PRIOR APPLICATION NUMBER:	09/313,942		
PRIOR FILING DATE:	1999-05-19		
PRIOR APPLICATION NUMBER:	60/101,858		
PRIOR FILING DATE:	1998-09-25		
NUMBER OF SEQ ID NOS:	32		
SOFTWARE:	FastSeq for Windows Version 3.0		
SEQ ID NO 24			
LENGTH:	1168		
TYPE:	PRT		
ORGANISM:	Homo sapiens		
US-09-313-942-24			
Query Match	61.2%;	Score 1783;	DB 2; Length 1168;
Best Local Similarity	99.7%;	Pred. No. 1.3e-148;	
Matches 330;	Conservative	1; Mismatches	0; Indels 0; Gaps 0;
Query	1	MLAVGCALLAALLAAPCAALAPRRCPAQEVARGVLTSLPGDVSVTILTCPCGVPEPNATVHM	60
		1	
		61	VLKPAAGSHPSRWAGMGRLLLRSLVQLHDSNGYCYRAGRAGTGHLLLVDPPEPQLS
		61	VLKPAAGSHPSRWAGMGRLLLRSLVQLHDSNGYCYRAGRAGTGHLLLVDPPEPQLS
		121	CFRKSPLSNVVCEWGPRSTPSLTTRKAVLLVRKFSQSPABDFQPCQYSOESQKFSQCLAV
		121	CFRKSPLSNVVCEWGPRSTPSLTTRKAVLLVRKFSQSPABDFQPCQYSOESQKFSQCLAV
		181	PEGDSSFYIVSMCVASSVGSKFSTQTFQCGGILQDPDPANITVTAVARNPWLVSVTWOD
		181	PEGDSSFYIVSMCVASSVGSKFSTQTFQCGGILQDPDPANITVTAVARNPWLVSVTWOD
		241	PHSWNSSFYRLRPELRYRAERSKFTFTVMVKDLQHHCVIHDWAGSLRHVVQLRAQBEFQ
		241	PHSWNSSFYRLRPELRYRAERSKFTFTVMVKDLQHHCVIHDWAGSLRHVVQLRAQBEFQ
		301	GEWSEWSPAMGTPWTESRSPPAENEVSPTM
		301	GEWSEWSPAMGTPWTESRSPPAENEVSPTM

Search completed: September 7, 2006, 23:04:45  
Job time : 51 secs

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RESULT 15
US-10-282-162-24
; Sequence 24, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-24

Query Match          61.2%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 1.3e-148;
Matches 330, Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY      1  MLAVGCALLAALLAAPGAALAPRCQAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60
;
;
;

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11/11/11

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:04:00 ; Search time 176 Seconds  
(without alignments)  
1455.442 Million cell updates/sec

Title: US-09-462-416A-13  
Perfect score: 2912  
Sequence: 1 MLVGCALLAALLAAGGAAL.....LILRSFKFLOSLRALRQM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2789	95.8	569	5	US-10-485-545A-14
2	1927.5	66.2	592	3	US-09-313-942-8
3	1927.5	66.2	592	3	US-09-313-942-8
4	1927.5	66.2	592	4	US-10-287-035-8
5	1927.5	66.2	592	4	US-10-287-035-8
6	1927.5	66.2	592	6	US-11-134-114-8
7	1917	65.8	468	4	US-10-247-463-12
8	1917	65.8	468	5	US-10-756-149-5377
9	1917	65.8	468	6	US-11-016-106-12
10	1910	65.6	360	3	US-09-313-942-15
11	1910	65.6	360	3	US-09-935-868-15
12	1910	65.6	360	4	US-10-287-035-15
13	1910	65.6	360	4	US-10-282-162-15
14	1910	65.6	360	6	US-11-134-114-15
15	1901	65.3	468	5	US-10-485-545A-11
16	1897	65.1	357	5	US-10-485-545A-13
17	1891	64.9	364	5	US-10-485-545A-10
18	1891	64.9	365	5	US-10-485-545A-12
19	1822.5	62.6	453	4	US-10-322-696-144
20	1789	61.4	1158	3	US-09-313-942-26
21	1789	61.4	1158	3	US-09-935-868-26
22	1789	61.4	1158	4	US-10-287-035-26
23	1789	61.4	1158	4	US-10-282-162-26
24	1789	61.2	1158	6	US-11-134-114-26
25	1783	61.2	1168	3	US-09-313-942-24
26	1783	61.2	1168	3	US-09-935-868-24
27	1783	61.2	1168	4	US-10-287-035-24

28	1783	61.2	1168	4	US-10-282-162-24	Sequence 24, Appl
29	1783	61.2	1168	6	US-11-134-114-24	Sequence 24, Appl
30	1683	57.8	315	3	US-09-313-942-16	Sequence 16, Appl
31	1683	57.8	315	3	US-09-935-868-16	Sequence 16, Appl
32	1683	57.8	315	4	US-10-282-035-16	Sequence 16, Appl
33	1683	57.8	315	4	US-10-282-162-16	Sequence 16, Appl
34	1683	57.8	315	6	US-11-134-114-16	Sequence 16, Appl
35	953.5	32.7	387	4	US-10-322-696-141	Sequence 141, Appl
36	953.5	32.7	460	4	US-10-247-463-13	Sequence 13, Appl
37	953.5	32.7	460	6	US-11-016-106-13	Sequence 13, Appl
38	952.5	32.7	266	6	US-11-043-788-194	Sequence 194, Appl
39	947.5	32.5	212	3	US-09-854-280-14	Sequence 14, Appl
40	947.5	32.5	212	3	US-09-854-208-14	Sequence 14, Appl
41	947.5	32.5	212	4	US-10-099-007A-3	Sequence 3, Appl
42	947.5	32.5	212	4	US-10-400-377-13	Sequence 13, Appl
43	947.5	32.5	212	4	US-10-400-708-13	Sequence 13, Appl
44	947.5	32.5	212	4	US-10-298-148-13	Sequence 13, Appl
45	947.5	32.5	212	4	US-10-440-464-61	Sequence 61, Appl

## ALIGNMENTS

RESULT 1  
US-10-485-545A-14  
; Sequence 14, Application US/10485545A  
; Publication No. US20050064558A1  
; GENERAL INFORMATION:  
; APPLICANT: University College Cardiff  
; TITLE OF INVENTION: A Fusion Protein  
; FILE REFERENCE: P102803PCT  
; CURRENT APPLICATION NUMBER: US/10/485,545A  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: 0119015.6  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 14  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: IL-6 fusion protein  
US-10-485-545A-14

Query Match	95.8%	Score 2789;	DB 5;	Length 569;
Best Local Similarity	96.1%	Pred. No. 9.4e-212;		
Matches 539;	Conservative	0;	Mismatches 12;	Indels 10;
Gaps 3;				
QY	1	MLVGCALLAALLAAGGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60	
DB	1	MLVGCALLAALLAAGGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60	
QY	61	VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS	120	
DB	61	VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS	120	
QY	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQQLAV	180	
DB	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQQLAV	180	
QY	191	PEGSSFFIVSMCVASSVSGSKFSTOTFGCGILQDPDPANITVTAVARNRWLSVTWOD	240	
DB	191	PEGSSFFIVSMCVASSVSGSKFSTOTFGCGILQDPDPANITVTAVARNRWLSVTWOD	240	
QY	241	PHSWNSSFYRLRFLRYRAERSKTFTTVMVKDLOHHCVTHDAWSGLRHVVQLRAQEFQ	300	
DB	241	PHSWNSSFYRLRFLRYRAERSKTFTTVMVKDLOHHCVTHDAWSGLRHVVQLRAQEFQ	300	
QY	301	GEWSWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVE---	357	
DB	301	GEWSWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPGRRR	360	

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Qy 358 -----FGAGLVILGGQFMPVPPGEDSKOVAAPHROPLTSSERIDKQIRYILDGISALRKET 412
Db 361 GSCGLGGGGGGGSLPVPVPPGEDSKOVAAPHROPLTSSERIDKQIRYILDGISA-RKET 419
Qy 413 CNKSNNCSSKALANNLNLPKMAEKDGCFCQSGFNSETCLVKIITGLLEFVYLYLQN 472
Db 420 CNKSNNCSSKALANNLNLPKMAEKDGCFCQSGFNSETCLVKIITGLLEFVYLYLQN 479
Qy 473 RFESSEQARAVQMSTKVLIQFQKAKNLDIAITTPDPTTNASLLTKLQAOQNWLQDMTT 532
Db 480 RFESSEQARAVQMSTKVLIQF-QKAKNLDIAITTPDPTTNASLLTKLQAOQNWLQDMTT 538
Qy 533 HLILRSFKFLOSSLRALRQM 553
Db 539 HLILRSFKFLOSSLRALRQM 559

RESULT 2
US-09-313-942-8
; Sequence 8, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-8

```

Query Match	66.2%	Score 1927.5	DB 3	Length 592
Best Local Similarity	72.8%	Pred. No. 1.6e-143		
Matches 391	Conservative 17	Mismatches 56	Indels 73	Gaps 8
Qy	1	MLAVGCALLAALAA	PGCAALAPRC	PAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db	1	MVAVGCALLAALAA	PGCAALAPRC	PAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy	61	VLKPAAGSHPSRWAGMGRRL	LLLSVQLHDSGNSCYRAGR	PAGTAVHLLVDVPPPEPQLS 120
Db	61	VLKPAAGSHPSRWAGMGRRL	LLLSVQLHDSGNSCYRAGR	PAGTAVHLLVDVPPPEPQLS 120
Qy	121	CFKRSPLSNVVCEWGP	STPSLTATKAVLLVRK	FQNSPAEDFQECQVSOEQSKESCQLAV 180
Db	121	CFKRSPLSNVVCEWGP	STPSLTATKAVLLVRK	FQNSPAEDFQECQVSOEQSKESCQLAV 180
Qy	181	PEGDSSFYIVSMCVASSV	SGSKFXTQTFQGGC	ILQPPANITVAVARNPRLSVTWQD 240
Db	181	PEGDSSFYIVSMCVASSV	SGSKFXTQTFQGGC	ILQPPANITVAVARNPRLSVTWQD 240
Qy	241	PHSNWSPFYRLRFLRYA	ERSKFTFTTWVKDLOHC	VIHDWAGSLRHVVQLRAQEEFGQ 300
Db	241	PHSNWSPFYRLRFLRYA	ERSKFTFTTWVKDLOHC	VIHDWAGSLRHVVQLRAQEEFGQ 300
Qy	301	GEWSEWPEAMGTPTWTS	RSRSPPAENEVSTPMQAL	TNNKDDNNILFRDSANATSLPVEFG- 359
Db	301	GEWSEWPEAMGTPTWTS	RSRSPPAENEVSTPMQAL	TNNKDDNNILFRDSANATSLPVQDAG 360
Qy	360	-----AGLVLGQ-----	FMPVPPGEDSKDVAAPHRQPL	-----TSSER 393
Db	361	EPKSCDTHTCPPCAP	PELLGSPSVFLPPKPK-----	KDTLMISRTPEVTVMVDVSHED 415

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Qy 394 IDKOIRVILDGI-----SALRKETCNKSNMCESSKEALAENNLN-----LPK 435
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 PEKFNWYVDGVEVHNAKTPREEQYNSTRVYVSVLTVLHQDMLNGKEYCKVSNKALPA 475
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 436 MAEKDGCFCQSGPNEE-----TCLVKITITGLIEFEFVYLYLQN 472
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

```

Query Match	66.2%	Score 1927.5	DB 3	Length 592
Best Local Similarity	72.8%	Pred. No. 1.6e-143		
Matches 391	Conservative 17	Mismatches 56	Indels 73	Gaps 8
Qy	1	MLVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60	
Db	1	MVAVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60	
Qy	61	VLKPAAGSHPSRWAGGRLLLRSLVQHDHSGNYSYRAGRPACTVHLLVDVPPPEPQLS	120	
Db	61	VLKPAAGSHPSRWAGGRLLLRSLVQHDHSGNYSYRAGRPACTVHLLVDVPPPEPQLS	120	
Qy	121	CFRKSPISNVVCEWGPSTPSLTATKAVLLVRKFNQSPAEQFQPCQYSQESQKFSQCLAV	180	
Db	121	CFRKSPISNVVCEWGPSTPSLTATKAVLLVRKFNQSPAEQFQPCQYSQESQKFSQCLAV	180	
Qy	181	PEGDSSFYIVSMCVASSVSGSKFTQFCGGIILQDPPANIITVAVARNPRLWLSVTWQD	240	
Db	181	PEGDSSFYIVSMCVASSVSGSKFTQFCGGIILQDPPANIITVAVARNPRLWLSVTWQD	240	
Qy	241	PHSNWSFYRLRFLRYAERSKFTFTVMVKDLQHCVIHDWAGSLRHVVQLRAQEEFGQ	300	
Db	241	PHSNWSFYRLRFLRYAERSKFTFTVMVKDLQHCVIHDWAGSLRHVVQLRAQEEFGQ	300	
Qy	301	GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIILFRSANATSLPVEFG-	359	
Db	301	GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIILFRSANATSLPVQDAG	360	
Qy	360	-----AGVLGGQ-----FMPVPPGEDSKDVAAPHRQL-----TSSER	393	
Db	361	EPKSCDKTHTCPCPAPBELIGGSPVFLPPKP-----KDTLMISRTPEVTCVVVDVSHED	415	
Qy	394	IDKIRYILDCI-----SALRKETCNKSNCESSKEALAEINNLT-----LPK	435	
Db	416	PEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPA	475	
Qy	436	MAEKDQCFQGSFNDE-----TCLVKITGLLISFEVYLEVLQN	472	
Db	476	PIEKTIKAKGPQREPOVYTLPPSRBELTKNQVSLTCLVK---GFYSDIAEVESN	529	

RESULT 4  
US-10-287-035-8  
; Sequence 8, Application US/10287035

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; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US99/0935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US99/09787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US99/09313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-8

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Query Match 66.2%; Score 1927.5; DB 4; Length 592;
Best Local Similarity 72.8%; Pred. No. 1.6e-143;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCALLAALAAPGAAAPRRCPAQEVARGVLTSLPGDSVTLTCTGVEPEDNATVHM 60
DB 1 MVAVGCALLAALAAPGAAAPRRCPAQEVARGVLTSLPGDSVTLTCTGVEPEDNATVHM 60

QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSEKQKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSEKQKSCQLAV 180

QY 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIILQDPDPANITTVAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIILQDPDPANITTVAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFLRYRAERSKTFTTMVKDLQHHCVIHDWGLRHVQLRAQEFGQ 300
DB 241 PHSWNSFYRLRFLRYRAERSKTFTTMVKDLQHHCVIHDWGLRHVQLRAQEFGQ 300

QY 301 GEWSWSPKMTPTWESRSPAEVSTPMQALTTNKDDNLLFRDSANATSLPVEFG- 359
DB 301 GEWSWSPKMTPTWESRSPAEVSTPMQALTTNKDDNLLFRDSANATSLPVEFG- 359

QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393
DB 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393

QY 394 IDKQIRYLDGI-----SALRKETCNKSNMCESSKEALAENLN-----LPK 435
DB 394 IDKQIRYLDGI-----SALRKETCNKSNMCESSKEALAENLN-----LPK 435

QY 416 PEVKFNWVDGVEVHNKTKPREQYNSTYRVSVTLVLDWGLNGKEYCKVSNKALPA 475
DB 416 PEVKFNWVDGVEVHNKTKPREQYNSTYRVSVTLVLDWGLNGKEYCKVSNKALPA 475

QY 436 MAEKDGCQSGFNEB-----TCLVKIITGLLEFEVLEYLQ 472
DB 436 MAEKDGCQSGFNEB-----TCLVKIITGLLEFEVLEYLQ 472

QY 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529
DB 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

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RESULT 5
US-10-282-162-8
; Sequence 8, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

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; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-8

Query Match 66.2%; Score 1927.5; DB 4; Length 592;
Best Local Similarity 72.8%; Pred. No. 1.6e-143;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCALLAALAAPGAAAPRRCPAQEVARGVLTSLPGDSVTLTCTGVEPEDNATVHM 60
DB 1 MVAVGCALLAALAAPGAAAPRRCPAQEVARGVLTSLPGDSVTLTCTGVEPEDNATVHM 60

QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSEKQKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFQNSPAEDFQPCQYSEKQKSCQLAV 180

QY 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIILQDPDPANITTVAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIILQDPDPANITTVAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFLRYRAERSKTFTTMVKDLQHHCVIHDWGLRHVQLRAQEFGQ 300
DB 241 PHSWNSFYRLRFLRYRAERSKTFTTMVKDLQHHCVIHDWGLRHVQLRAQEFGQ 300

QY 301 GEWSWSPKMTPTWESRSPAEVSTPMQALTTNKDDNLLFRDSANATSLPVEFG- 359
DB 301 GEWSWSPKMTPTWESRSPAEVSTPMQALTTNKDDNLLFRDSANATSLPVEFG- 359

QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393
DB 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393

QY 394 IDKQIRYLDGI-----SALRKETCNKSNMCESSKEALAENLN-----LPK 435
DB 394 IDKQIRYLDGI-----SALRKETCNKSNMCESSKEALAENLN-----LPK 435

QY 416 PEVKFNWVDGVEVHNKTKPREQYNSTYRVSVTLVLDWGLNGKEYCKVSNKALPA 475
DB 416 PEVKFNWVDGVEVHNKTKPREQYNSTYRVSVTLVLDWGLNGKEYCKVSNKALPA 475

QY 436 MAEKDGCQSGFNEB-----TCLVKIITGLLEFEVLEYLQ 472
DB 436 MAEKDGCQSGFNEB-----TCLVKIITGLLEFEVLEYLQ 472

QY 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529
DB 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

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RESULT 6
US-11-134-114-8
; Sequence 8, Application US/11134114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22

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; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-134-114-8

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Query Match	56.2%	Score 1927.5	DB 6	Length 592	
Best Local Similarity	72.8%	Pred. No. 1.6e-143			
Matches 391	Conservative	17	Mismatches 56	Indels 73	Gaps 8
QY	1	MLAVGCALLAALAAACGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW	60		
DB	1	MVAVGCALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW	60		
QY	61	VLKPAAGSHPSRWAGGRLLLRSLVQHDPSGNYSCYRAGRPAGTCHLLVDVPPPEEQLS	120		
DB	61	VLKPAAGSHPSRWAGGRLLLRSLVQHDPSGNYSCYRAGRPAGTCHLLVDVPPPEEQLS	120		
QY	121	CFRKSPLSNVVCEWGPSTSLTKAVLLVRKFNQSPAEQFQPCQYQSQESKFSQCLAV	180		
DB	121	CFRKSPLSNVVCEWGPSTSLTKAVLLVRKFNQSPAEQFQPCQYQSQESKFSQCLAV	180		
QY	181	PEGDSFPYIVSMCVASSVSGSKFTQTFQGGCILQDPPANITVTAVARNPRLWSVTWQD	240		
DB	181	PEGDSFPYIVSMCVASSVSGSKFTQTFQGGCILQDPPANITVTAVARNPRLWSVTWQD	240		
QY	241	PHSWNSFYRLRFELRYRAERSKFTFTMMVKDLQHCVIHDWAGSLRHVQLRAEQEFGQ	300		
DB	241	PHSWNSFYRLRFELRYRAERSKFTFTMMVKDLQHCVIHDWAGSLRHVQLRAEQEFGQ	300		
QY	301	GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVBFQ	359		
DB	301	GEWSEWSPGAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG	360		
QY	360	-----AGLVLGQ-----FMPVPPEGDSKDVAAPHRQPL-----TSSER	393		
DB	361	EPKSCDKTHCTPCCPAPELJGGRESVFLPPPKP-----KTLMIISRTPEVTCVVVDVSHED	415		
QY	394	IDQIRYILDG1-----SALRKETCNKSNCESSKEALAEINLN-----LPK	435		
DB	416	PEVKFNWYDGVVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPA	475		
QY	436	MAEKDGCFCQGGFNEE-----TCLVKITGLLSTFVEVLYQLON	472		
DB	476	PIKTIKSKAQGPQEPQVYLTPLPSRDELTKNOVSLTKLVK---GFPSDIAVAWESN	529		

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RESULT 7
US-10-247-463-12
/ Sequence 12, Application US/10247463
/ Publication No. US20030082734A1
/ GENERAL INFORMATION:
/ APPLICANT: Dowling, Lynette M.
/ APPLICANT: Timans, Jacqueline C.
/ APPLICANT: Gormen, Daniel M.
/ APPLICANT: Kastelein, Robert A.
/ APPLICANT: Bazan J. Fernando
/ TITLE OF INVENTION: Mammalian Recep
/ TITLE OF INVENTION: Methods
/ FILE REFERENCE: DX0992Q
/ CURRENT APPLICATION NUMBER: US/10/2
/ CURRENT FILING DATE: 2002-09-18
/ PRIOR APPLICATION NUMBER: US/09/588
/ PRIOR FILING DATE: 2000-05-31
/ NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12a
; LENGTH: 468
; TYPE: PRT
; ORGANISM: primate
US-10-247-463-12

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Query Match 65.8%; Score 1917; DB 4; Length 468;  
Best Local Similarity 96.8%; Pred. No. 7.8e-143;  
Matches 360; Conservative 2; Mismatches 4; Indels

Qy	1	MLAVGCALLAALLAAPGAALAPRCPRAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM	60
Db	1	MLAVGCALLAALLAAPGAALAPRCPRAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM	60
Qy	61	VLKPAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPOL	120
Db	61	VLKPAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPOL	120
Qy	121	CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFKONSAPAEDFQEPQCYSQESQKFSQCLAV	180
Db	121	CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFKONSAPAEDFQEPQCYSQESQKFSQCLAV	180
Qy	181	PEGDSSEYIYVSMCMVASSVGSKFSKTQTFQGGCIIQDPDPANITVTAVARNPRLWSVTWOD	240
Db	181	PEGDSSEYIYVSMCMVASSVGSKFSKTQTFQGGCIIQDPDPANITVTAVARNPRLWSVTWOD	240
Qy	241	PHSNSSFYRLRPELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVOLRAQEEFQ	300
Db	241	PHSNSSFYRLRPELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVOLRAQEEFQ	300
Qy	301	GEWSEWPEAMGTPTWTSRSPPEAENESTPMQALTTNKDDNNILFRDSANATSLSPVEFGA	360
Db	301	GEWSEWPEAMGTPTWTSRSPPEAENESTPMQALTTNKDDNNILFRDSANATSLSPVQDSS	360
Qy	361	G-----LVLGG 366	
Db	361	SVPLPTFLVAGG 372	

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RESULT 8
US-10-756-149-5377
; Sequence 5377, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aiziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF
; TITLE OF INVENTION: METHODS OF SCREENING
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5377
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5377

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	Query Match	65.8%	Score 1917;	DB 5;	Length 468;	
	Best Local Similarity	96.8%;	Pred. No. 7.8e-143;			
	Matches 360;	Conservative 2;	Mismatches 4;	Indels 6;	Gaps 1;	
<hr/>						
Qy	1	MLAVGCALLAALIAAPCAALAPRCPAQEVARGLVTSLPDGSVTLTCPGVEPDNATVHW	60			
Dd	1	MLAVGCALLAALIAAPCAALAPRCPAQEVARGLVTSLPDGSVTLTCPGVEPDNATVHW	60			
<hr/>						
Qy	61	VLRKPAAGSHPSRWAGRGRELLRSVOLHDSGNYSYVRAGRPGAGTGHLLVDVPPEEPQLS	120			
Dd	61	VLRKPAAGSHPSRWAGRGRELLRSVOLHDSGNYSYVRAGRPGAGTGHLLVDVPPEEPQLS	120			
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Qy	121	CFRKSPLSNVVCEWGPGRSTPSLTKAVLLVRKFQNSPAEDFQBPCQYSQBSQKFSCLAV	180			

Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Qy 301 GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFGA 360  
Db 301 GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDQSS 360  
Qy 361 G-----LVLG 366  
Db 361 SVPLPTFLVAGG 372

## RESULT 9

US-11-016-106-12  
; Sequence 12, Application US/11016106  
; Publication No. US20050106673A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Lynette M.  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and  
; FILE OF INVENTION: Methods  
; FILE REFERENCE: DX09920  
; CURRENT APPLICATION NUMBER: US/11/016,106  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: primate  
US-11-016-106-12

Query Match 65.8%; Score 1917; DB 6; Length 468;  
Best Local Similarity 96.8%; Pred. No. 7.8e-143;  
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;  
Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60  
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTAVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTAVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Qy 301 GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFGA 360  
Db 301 GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDQSS 360

Qy 361 G-----LVLG 366  
Db 361 SVPLPTFLVAGG 372

## RESULT 10

US-09-313-942-15  
; Sequence 15, Application US/09313942  
; Publication No. US20020012962A1  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens.  
US-09-313-942-15

Query Match 65.6%; Score 1910; DB 3; Length 360;  
Best Local Similarity 99.4%; Pred. No. 1.9e-142;  
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60  
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60  
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTAVHLLVDVPPPEPQLS 120  
Db 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTAVHLLVDVPPPEPQLS 120  
Qy 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180  
Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180  
Qy 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Db 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVTAVARNPRWLSVTWQD 240  
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300  
Qy 301 GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357  
Db 301\*GEWSWSPSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEQ 357

## RESULT 11

US-09-935-868-15  
; Sequence 15, Application US/09935868  
; Patent No. US20020164690A1  
; GENERAL INFORMATION:  
; APPLICANT: Regeneron Pharmaceuticals, Inc  
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
; FILE REFERENCE: REG 203D  
; CURRENT APPLICATION NUMBER: US/09/935,868  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 360

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match      65.6%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEPEPNATVHW 60
Db 1 MVAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEPEPNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120
Db 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300

Qy 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357
Db 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 12
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: NEIL STAHL AND GEORGE D. YANCOPOULOS
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match      65.6%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEPEPNATVHW 60
Db 1 MVAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEPEPNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120
Db 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300

Qy 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357
Db 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 13
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT 4
; ORGANISM: Homo sapiens
US-10-282-162-15

Query Match      65.6%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEPEPNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120
Db 61 VLKPAAGSHPSRWAGMRLLRSVLQHDGSGNSCYRAGRPACTVHLLVDVPEEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSQKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWMSGLRHVVQLRAQEEFGQ 300

Qy 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357
Db 301 GESEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 14
US-11-134-114-15
; Sequence 15, Application US/11134114
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; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-15

Query Match      65.6%; Score 1910; DB 6; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVAVGCALLAALAPGAALAPRRCPAQAEVARGVLTSLPGDSVTLTCFVPEPNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEQFQPCQYSEKQKFCOLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEQFQPCQYSEKQKFCOLAV 180

Qy 181 PEGDSSFFIYVSMCVASSVGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFFIYVSMCVASSVGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEERFQ 300
   :|||||
Db 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEERFQ 300

Qy 301 GEWSEWSPKMGTPWTESRSPAEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
   :|||||
Db 301 GEWSEWSPKMGTPWTESRSPAEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 15
US-10-485-545A-11
; Sequence 11, Application US/10485545A
; Publication No. US20050064558A1
; GENERAL INFORMATION:
; APPLICANT: University College Cardiff
; APPLICANT: University of Wales College of Medicine
; TITLE OF INVENTION: A Fusion Protein
; FILE REFERENCE: P102803PCT
; CURRENT APPLICATION NUMBER: US/10/485,545A
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: 0119015.6
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 468
; TYPE: PRT

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; ORGANISM: homo sapien
US-10-485-545A-11

Query Match      65.3%; Score 1901; DB 5; Length 468;
Best Local Similarity 96.2%; Pred. No. 1.4e-141;
Matches 358; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

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Db 1 MLAVGCALLAALAPGAALAPRRCPAQAEVARGVLTSLPGDSVTLTCFVPEPNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEQFQPCQYSEKQKFCOLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEQFQPCQYSEKQKFCOLAV 180

Qy 181 PEGDSSFFIYVSMCVASSVGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFFIYVSMCVASSVGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEERFQ 300
   :|||||
Db 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEERFQ 300

Qy 301 GEWSEWSPKMGTPWTESRSPAEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360
   :|||||
Db 301 GEWSEWSPKMGTPWTESRSPAEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360

Qy 361 G-----LVLG 366
   :|||
Db 361 SVPLPTFLVAGG 372

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Job time : 17g secs

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10/15/01

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 23:05:01 ; Search time 34 Seconds  
(without alignments)  
1142.592 Million cell updates/sec

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Perfect score: 2912  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	947.5	32.5	212	6	US-10-933-854-11
5	927	31.8	183	7	US-11-330-917-198
6	912.5	31.3	454	6	US-10-669-920-1402
7	907	31.1	277	6	US-10-669-920-1405
8	296	10.2	368	6	US-10-449-902-38075
9	201	6.9	422	7	US-11-296-092-32
10	201	6.9	422	7	US-11-296-155-32
11	201	6.9	422	7	US-11-300-928-27
12	198.5	6.8	328	7	US-11-234-676-4
13	164.5	5.6	918	7	US-11-275-181-6
14	158.5	5.4	335	7	US-11-234-676-321
15	155	5.3	306	6	US-10-669-920-93
16	155	5.3	604	6	US-10-669-920-95
17	149	5.1	890	6	US-10-553-520-180
18	139	4.8	229	7	US-11-297-134-8
19	139	4.8	229	7	US-11-275-181-5
20	138	4.7	268	6	US-10-669-920-104
21	138	4.7	347	6	US-10-669-920-108
22	138	4.7	374	6	US-10-669-920-110
23	138	4.7	618	6	US-10-669-920-112
24	135	4.6	324	7	US-11-353-451-10
25	135	4.6	519	7	US-11-301-764-71

26	135	4.6	519	7	US-11-353-427-6	Sequence 6, Appli
27	135	4.6	519	7	US-11-353-454-6	Sequence 6, Appli
28	135	4.6	662	7	US-11-301-764-5	Sequence 5, Appli
29	135	4.6	662	7	US-11-353-451-8	Sequence 8, Appli
30	135	4.6	732	7	US-11-353-451-6	Sequence 6, Appli
31	135	4.6	764	7	US-11-301-764-39	Sequence 39, Appli
32	133.5	4.6	885	6	US-10-505-928-432	Sequence 432, App
33	133.5	4.6	885	7	US-11-251-465-20	Sequence 20, Appl
34	129	4.4	894	7	US-11-251-465-21	Sequence 21, Appl
35	128	4.4	970	7	US-11-301-764-120	Sequence 120, App
36	124.5	4.3	239	7	US-11-353-451-12	Sequence 12, Appl
37	120	4.1	440	7	US-11-251-465-65	Sequence 65, Appl
38	120	4.1	449	7	US-11-251-465-68	Sequence 68, Appl
39	119	4.1	4391	7	US-11-183-325-56	Sequence 56, Appl
40	118.5	4.1	771	7	US-11-234-587-325	Sequence 325, App
41	115.5	4.0	635	6	US-10-548-727-10	Sequence 10, Appl
42	115	3.9	536	6	US-10-669-920-305	Sequence 305, App
43	115	3.9	536	6	US-10-669-920-307	Sequence 307, App
44	114.5	3.9	635	6	US-10-511-937-2424	Sequence 2424, Ap
45	114.5	3.9	635	6	US-10-548-727-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-10-669-920-1407  
; Sequence 1407, Application US/10669920  
; GENERAL INFORMATION:  
; APPLICANT: Malandro, Marc S.  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
; FILE REFERENCE: 20366-066001  
; CURRENT APPLICATION NUMBER: US/10/669,920  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: US 10/004,113  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 10/052,482  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/997,722  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 10/034,650  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 10/085,117  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 10/087,192  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 10/322,281  
; PRIOR FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US 10/322,696  
; PRIOR FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 1441  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1407  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-669-920-1407

Query Match	64.3%	Score 1871;	DB 6;	Length 464;
Best Local Similarity	95.4%	Pred. No. 5.8e-135;		
Matches 355;	Conservative 2;	Mismatches 5;	Indels 10;	Gaps 3;
QY	1	MLAVGCALLAALLAAGAALAPRRCPAQEVARGVLTSLPGDSVTITCPGVEPEDNATVHW	60	
Db	1	MLAVGCALLAALLAAGA--APRRCPAQEV--VLTSLPGDSVTITCPGVEPEDNATVHW	56	
QY	61	VLRKPAAGSHPSRWAGMGRLLLRSLVQLHDSGNYSCYRAGRPAGTTHLLVDVPPPEPOLLS	120	
Db	57	VLRKPAAGSHPSRWAGMGRLLLRSLVQLHDSGNYSCYRAGRPAGTTHLLVDVPPPEPOLLS	116	
QY	121	CFRKSPLSNVCEWGPRTPTSLTTKAVLLVRKFQNSPAEDFQEPCCQYSQESQKFSQCLAV	180	

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Db 117 CFRKSPNVVCEMGPRSTSLTTKAVLLVRKFQNSPAEDQBEPCQYSQSSQKSCQLAV 176
Qy 181 PEGDSSFYIVCMVASSVSGSKFTQTQFQGGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Db 177 PEGDSSFYIVCMVASSVSGSKFTQTQFQGGIILQPPPPANITVTAVARNPRWLSVTWQD 236
Qy 241 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Db 237 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVQLRAQEBFGQ 296
Qy 301 GEWSEWPEAMGTPTWTSRSPAPNEVSTPMQALTTNNKDDNIIILFRSANATSLPVEFGA 360
Db 297 GEWSEWPEAMGTPTWTSRSPAPNEVSTPMQALTTNNKDDNIIILFRSANATSLPVDSS 356
Qy 361 G-----LVLGG 366
Db 357 SVPLPTFLVAGG 368

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RESULT 2
US-10-505-928-453
; Sequence 453, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 453
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-453

```

```

Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVLGGQF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSGLLLVLPAAFPAPVPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRPESSEQARAVQMSKVLITQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMT 531
Db 131 NRPESSEQARAVQMSKVLITQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMT 190
Qy 532 THLILRSFKFQSSLRALRQM 553
Db 191 THLILRSFKFQSSLRALRQM 212

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RESULT 3
US-10-511-937-2489
; Sequence 2489, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald

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; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2489
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2489

```

```

Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVLGGQF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSGLLLVLPAAFPAPVPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRPESSEQARAVQMSKVLITQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMT 531
Db 131 NRPESSEQARAVQMSKVLITQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMT 190
Qy 532 THLILRSFKFQSSLRALRQM 553
Db 191 THLILRSFKFQSSLRALRQM 212

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RESULT 4
US-10-933-854-11
; Sequence 11, Application US/10933854
; Publication No. US20060105347A1
; GENERAL INFORMATION:
; APPLICANT: GTC Biotherapeutics, Inc.
; APPLICANT: Meade, Harry
; APPLICANT: Cox, Geoffrey F.
; TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammals
; FILE REFERENCE: GTC-220 PCT
; CURRENT APPLICATION NUMBER: US/10/933,854
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/500,910
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Human a Interferon Variant 2A
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/EMBL/DBJ Accession No. CAA00839
; DATABASE ENTRY DATE: 1993-12-03
; RELEVANT RESIDUES: (1)..(212)
US-10-933-854-11

```

```

Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;

```



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; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-1405

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Query Match 31.1%; Score 907; DB 6; Length 277;
Best Local Similarity 93.4%; Pred. No. 1.1e-61;
Matches 169; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 192 MCVASSVGSKESKQTQGGCIGLOPPANITVTAVARNPRLSVTWQDHSWNSSEYRL 251
Db 1 MCVASSVGSKESKQTQGGCIGLOPPANITVTAVARNPRLSVTWQDHSWNSSEYRL 60

Qy 252 RFLRYRAERSKTTTVMVKDQHCIVHDWSGLRHVVQLRAQEEFGQGSWSESPAM 311
Db 61 RFLRYRAERSKTTTVMVKDQHCIVHDWSGLRHVVQLRAQEEFGQGSWSESPAM 120

Qy 312 GTPWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGAG-----LVLG 365
Db 121 GTPWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGAG-----LVLG 365

Qy 366 G 366
Db 181 G 181

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RESULT 8
US-10-449-902-38075
; Sequence 38075, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38075
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38075
Query Match 10.2%; Score 296; DB 6; Length 368;

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Best Local Similarity 28.0%; Pred. No. 7.1e-15;
Matches 106; Conservative 45; Mismatches 152; Indels 76; Gaps 16;

Qy 12 LLAAPGAALAPRRCPAQEVARGVLTSLPGDSVLTLCFGEVPEPDNATVHVWLKPAAGSHP 71
Db 12 VLAAGVVAQRH---SQQDTHVLYERLGSVDVLPD- -GTAAGTAVTWVNGTDLAAHY 67

Qy 72 SRWAGMRLLRLRSVQLHDSGNSYCVRAG-----RPAGTVHLLVDVPEEPOLSCFRKSPL 127
Db 68 N-----GSQLVLEGLDLSHSGHYACYGQSSWHLRYQALLH--VGMPPREPVLTCRSNSYP 120

Qy 128 SNVVCWE---GPRSTPSLTITKAVLLYRK- -QNSPAEDFQEPQCYQSQKFSQCLAVP 181
Db 121 KGFYCSMHLPSPTPIPTNTFNVTVLHSGKLGCGRDPA-----PKRCHIRYT 167

Qy 182 EGDSSF-YIVSMCVASSVGSKFSKQTOTFCQCGILQDPPANITVTAVARNPRLSVTWQD 240
Db 168 HLFSTVKYKVTLTVTNALGHN-STAITFDEFTIVKDPDPENNVVARPVSPRRLLEVWTQ 226

Qy 241 PHSW-NSSFYRLRFLRYRAERSKTTTVMVKDQHC-----VIHDAWSGLRHVVQ 291
Db 227 PSSWPDPEFPKFLRYRP-----LILDQWQHVELSDGTTHTTIDYAGKBYIIQ 277

Qy 292 LRAQEEFGQGSWSESPAMGTPM-----TESRSPPAENEVSTPMQALTTNKDDDDNI 343
Db 278 VAKDN-EIGTSDWSVAHAHATWTEPRYLTTAQAPETTTTTTSFVPPPTKICD-- 334

Qy 344 LFRDSANATSLPVEFGAGL 362
Db 335 -----PGEVGDGV 342

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RESULT 9
US-11-296-092-32
; Sequence 32, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

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; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3.1
; SEQ ID NO 27
; LENGTH: 422
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-300-928-37

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Query Match 6.9%; Score 201; DB 7; Length 422;  
Best Local Similarity 24.7%; Pred. No. 1.5e-07;  
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

Query Match	6.8%	Score 198.5	DB 7	Length 328	
Best Local Similarity	24.1%	Pred. No. 1.7e-07			
Matches	81	Conservative 51	Mismatches 135	Indels 69	Gaps 14
Qy	13	LAAPGAALAPRRCPAQEAVARGVLTSLPDGSVTLITPCGVEPEDNATVHWLRKPAAGSHPS	72		
Db	16	LASPLVAIWELKXDVVVELDWTVPDAPGEMVLTCDTPE--EDGIT--WTL-----DOSS	66		
Qy	73	RWAGMGRLLLRSVQLHSDNSCYCGRAGPAGTVHLLV-----DV-----PPEE	116		
Db	67	EVLGSGKTLTIQVKEFGDAQYTCHKGGVLSHLLHKKEDGIWSTDILKDQKEPKVK	126		
Qy	117	PQUSCFRPSPLSNVCEW-----GPRSTPSLTTKVALLVRKFNQNSPAED	160		
Db	127	TFURCEAKNYSGRFTCWMLTTITDITFYSVKSRGSSDPQOVCGAATLSAERVGDNKE	186		
Qy	161	FQEPCCOYSQBSQFSCOLAVPEGDSSFYIVSMCVASSVGSKFSKTOTFOGGGILQPDPPA	220		
Db	187	Y-----EYSVEQEDS---ACPAAEESLPLEWVDVAVHKLKYENTSSFFTRDIIXPDPPK	239		
Qy	221	NITVTAVARNPRLVSWTQDPHWSNS--SFYRLRF--ELRYAERSKRTFTTMMVKDLQHH	276		
Db	240	NLQKLPL-KNSRQVEVSWEPDWTSPHPSYFSLTFCVQVQGKSKREK-----KDR----	288		
Qy	277	CVTHDAWSGL-----RHHVOLRAQEEFGQGEWSWS	307		
Db	289	-VFDTKTSATVICRKNASISVRAODRYYSSSWSGEWA	323		



```
RESULT 14
US-11-234-676-321
; Sequence 321, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; TITLE OF INVENTION: Autoimmune Disease Therapeutics
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 321
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-234-676-321

Query Match          5.4%; Score 158.5; DB 7; Length 335;
Best Local Similarity 21.1%; Pred. No. 0.0002;
Matches 68; Conservative 51; Mismatches 113; Indels 91; Gaps 15;

QY 39 PGDSVTLCPGVEPDNATVHWV--LRKPAAGSHPSRWAGMGRRLLRSLVQLHDSGNYS 96
Db 42 PGETVNLTCDTPEEDD---ITWTSQRHGVIQS-----GKLTITVKEFLDAGQYTC 90
QY 97 YRAGRPACTVHLLVDVP-----PEEPOLSCFRKSPLSNVVCEW----- 134
Db 91 HKGETLSHLLHKKENGISWTEILKNFKNTFLKCEAPNYSGRFTCSMLVQRNMDLK 150
QY 135 ----GPRSTP-----SLTTKAVLLVRKFQNSPAEDFQEPQCYSQSKFSCQ--L 178
Db 151 FNIKSSSSSPDSRAVTCGMASLSAEKVTL-----DQDYKYSVSCQBDV 195
QY 179 AVPEGDSSFYIVSMCVASSVSGSKFSTOT--FOGCGILOPDPANITVTAVARNPRLSVT 237
Db 196 TCTPAEETLPI--ELALEARQQNKYENYSTSFIRDIIRKPPDKNLQMKPLKNSQ--VEVS 252
QY 238 WQDPHSNNS--SFYRLRFLRYRAERSKTFITTMVKDLQHCVHIDAW-----S 284
Db 253 WEYDPSMTSPHSYSLKFFVRLQRKKEK-----MKETEEGCNQKGAFLVEKTSVEVQCK 306
QY 285 GLRHVVQLRAQEFGQGEWSEWS 307
Db 307 GGNVCVQ--AQDRYNNSSCSKWA 327

RESULT 15
US-10-669-920-93
; Sequence 93, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
```

```
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-93

Query Match          5.3%; Score 155; DB 6; Length 306;
Best Local Similarity 22.6%; Pred. No. 0.00032;
Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

QY 113 PPEPQLSCFRKSPLSNVVCEWGRPRSTPSLTTKAVLLVRKFQNSPAEDFQEPQCYSQ 172
Db 20 PPGKPEIHKCRSPDKETFTTCWNNPGSGGLPTNYSL-----TYSKEGE 62
QY 173 K--FSCQLAVPEGDSS-----FYIVSMCVASSVSGSKFSTOTTFQCGILOPDP 218
Db 63 KNTYECPDYKTSNGNSCFKQYTSIKWIIYIITVNATNMGSSSTSDPLYVDVTVIVEPEP 122
QY 219 PANIT--VTAVARNPRLSVTWQDP--HSMNSSFYRLRFLRYRAERSKTFITTMVKLOLQ 274
Db 123 PRNLTLEVQLKDKKTYLWVKWLPPPTITDVKTGWFTMEYELRKSEEA---DEWEIHFTG 179
QY 275ΔHHC--VIHDAWSGLRHVVQLRAQEFGQGEWSEWSPE 309
Db 180 HQTQPKVPDLYPGQKYLVTQCKPD--HGYWSRWQGE 214

Search completed: September 7, 2006, 23:08:26
Job time : 36 secs
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